



#3

Sequence Listing

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Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
Paoni, Nicholas F.

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 Gln Pro Arg Asp Pro Val Arg Pro Pro Arg Arg Gly Arg Gly Pro
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 65 70 75
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 gccagcagct ttgcaagact ttttattgtt gaaacagaaa gcagagctgg 1050
 ctaatcccaa ggcagtgtga ctgagctaac caccaatgtc tctccagga 1100
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 agggagtccc accatcgtct gtggtatccc agggctcctg ctcaagtttt 1250
 ctttgaaaag gagggctgga atggtacatc acataggcaa gtctgccc 1300
 gtatttaggc tttgctgtct tgggtgtgat taagggaat tgaaagaatt 1350
 gccattcaa aatgatcttt accgtggcct gcccatgct tatggctccc 1400
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 taaaagataa gtcaacccaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaa 1508

<210> 10
<211> 319
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-17
<223> Signal Peptide

<220>
<221> misc_feature
<222> 36-47, 108-113, 166-171,198-203, 207-212
<223> N-myristoylation Sites.

<220>
<221> misc_feature
<222> 39-42
<223> Glycosaminoglycan Attachment Site.

<220>
<221> TRANSMEM
<222> 136-152
<223> Transmembrane Domain

<220>
<221> misc_feature
<222> 161-163, 187-190 and 253-256
<223> N-glycosylation Sites.

<400> 10
Met Leu Phe Trp Val Leu Gly Leu Leu Ile Leu Cys Gly Phe Leu
1 5 10 15

Trp Thr Arg Lys Gly Lys Leu Lys Ile Glu Asp Ile Thr Asp Lys
20 25 30

Tyr Ile Phe Ile Thr Gly Cys Asp Ser Gly Phe Gly Asn Leu Ala
35 40 45

Ala Arg Thr Phe Asp Lys Lys Gly Phe His Val Ile Ala Ala Cys
50 55 60

Leu Thr Glu Ser Gly Ser Thr Ala Leu Lys Ala Glu Thr Ser Glu
65 70 75

Arg Leu Arg Thr Val Leu Leu Asp Val Thr Asp Pro Glu Asn Val
80 85 90

Lys Arg Thr Ala Gln Trp Val Lys Asn Gln Val Gly Glu Lys Gly
95 100 105

Leu Trp Gly Leu Ile Asn Asn Ala Gly Val Pro Gly Val Leu Ala
110 115 120

Pro Thr Asp Trp	Leu Thr Leu Glu Asp	Tyr Arg Glu Pro Ile Glu
125	130	135
Val Asn Leu Phe Gly	Leu Ile Ser Val Thr	Leu Asn Met Leu Pro
140	145	150
Leu Val Lys Lys Ala	Gln Gly Arg Val Ile	Asn Val Ser Ser Val
155	160	165
Gly Gly Arg Leu Ala	Ile Val Gly Gly Gly	Tyr Thr Pro Ser Lys
170	175	180
Tyr Ala Val Glu Gly	Phe Asn Asp Ser Leu	Arg Arg Asp Met Lys
185	190	195
Ala Phe Gly Val His	Val Ser Cys Ile Glu	Pro Gly Leu Phe Lys
200	205	210
Thr Asn Leu Ala Asp	Pro Val Lys Val Ile	Glu Lys Lys Leu Ala
215	220	225
Ile Trp Glu Gln Leu	Ser Pro Asp Ile Lys	Gln Gln Tyr Gly Glu
230	235	240
Gly Tyr Ile Glu Lys	Ser Leu Asp Lys Leu	Lys Gly Asn Lys Ser
245	250	255
Tyr Val Asn Met Asp	Leu Ser Pro Val Val	Glu Cys Met Asp His
260	265	270
Ala Leu Thr Ser Leu	Phe Pro Lys Thr His	Tyr Ala Ala Gly Lys
275	280	285
Asp Ala Lys Ile Phe	Trp Ile Pro Leu Ser	His Met Pro Ala Ala
290	295	300
Leu Gln Asp Phe Leu	Leu Leu Lys Gln Lys	Ala Glu Leu Ala Asn
305	310	315
Pro Lys Ala Val		

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
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 ggccttggg cgcgcgcac cactgtagtc atgtaccac cgcgcgcgc 150
 gcgcctcat cgggaattca tctcggtgac gctgagcttt ggcgagagct 200

atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttcctcc ttgcctttct 300
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 ggggttaaac cagcaaacc acccgtctta ccagctctc agaaggcgga 450
 caccgacct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct caoctgcaga ttagacccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600
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 gagcggatg cgagcctgag cagggcaccg agctcccttc aagaagagca 700
 gaagtgcaca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
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 catggaaagg ataccgcaag ttgcatggg gccatgacga gctgaagcct 850
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgatcga 900
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 cacatccag gctgtctgg gaagaaggat gggtggtgc ccatgttcat 1350
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 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
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 ggtgaccgag tggacagccc aggggtgcagc tctgcacggg ctggtgaagc 2500
 ctcagatgtc cccaatccaa gggctcggag gggctgcctg gactccagag 2550
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 cctcctggcc gcccgcagg gggcttggag ggctggacgg caagtccgtc 2650
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 ttgatttgct ctaaccgcaa 2720

<210> 12

<211> 699

<212> PRT

<213> Homo sapiens

<220>

<221> TRANSMEM

<222> 21-40 and 84-105

<223> Transmembrane Domain (type II)

<400> 12

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Gln Ser Asp Phe	Leu Thr Pro Pro	Val Gly Gly Ala	Pro Trp Ala
	20	25	30
Val Ala Thr Thr	Val Val Met Tyr	Pro Pro Pro Pro	Pro Pro
	35	40	45
His Arg Asp Phe	Ile Ser Val Thr	Leu Ser Phe Gly	Glu Ser Tyr
	50	55	60
Asp Asn Ser Lys	Ser Trp Arg Arg	Arg Ser Cys Trp	Arg Lys Trp
	65	70	75
Lys Gln Leu Ser	Arg Leu Gln Arg	Asn Met Ile Leu	Phe Leu Leu
	80	85	90
Ala Phe Leu Leu	Phe Cys Gly Leu	Leu Phe Tyr Ile	Asn Leu Ala
	95	100	105
Asp His Trp Lys	Ala Leu Ala Phe	Arg Leu Glu Glu	Glu Gln Lys
	110	115	120
Met Arg Pro Glu	Ile Ala Gly Leu	Lys Pro Ala Asn	Pro Pro Val
	125	130	135
Leu Pro Ala Pro	Gln Lys Ala Asp	Thr Asp Pro Glu	Asn Leu Pro
	140	145	150
Glu Ile Ser Ser	Gln Lys Thr Gln	Arg His Ile Gln	Arg Gly Pro
	155	160	165
Pro His Leu Gln	Ile Arg Pro Pro	Ser Gln Asp Leu	Lys Asp Gly
	170	175	180
Thr Gln Glu Glu	Ala Thr Lys Arg	Gln Glu Ala Pro	Val Asp Pro
	185	190	195
Arg Pro Glu Gly	Asp Pro Gln Arg	Thr Val Ile Ser	Trp Arg Gly
	200	205	210
Ala Val Ile Glu	Pro Glu Gln Gly	Thr Glu Leu Pro	Ser Arg Arg
	215	220	225
Ala Glu Val Pro	Thr Lys Pro Pro	Leu Pro Pro Ala	Arg Thr Gln
	230	235	240
Gly Thr Pro Val	His Leu Asn Tyr	Arg Gln Lys Gly	Val Ile Asp
	245	250	255
Val Phe Leu His	Ala Trp Lys Gly	Tyr Arg Lys Phe	Ala Trp Gly
	260	265	270
His Asp Glu Leu	Lys Pro Val Ser	Arg Ser Phe Ser	Glu Trp Phe
	275	280	285
Gly Leu Gly Leu	Thr Leu Ile Asp	Ala Leu Asp Thr	Met Trp Ile

	290		295		300
Leu Gly Leu Arg	Lys Glu Phe Glu Glu	Ala Arg Lys Trp Val	Ser		
	305		310		315
Lys Lys Leu His	Phe Glu Lys Asp Val	Asp Val Asn Leu Phe	Glu		
	320		325		330
Ser Thr Ile Arg	Ile Leu Gly Gly Leu	Leu Ser Ala Tyr His	Leu		
	335		340		345
Ser Gly Asp Ser	Leu Phe Leu Arg Lys	Ala Glu Asp Phe Gly	Asn		
	350		355		360
Arg Leu Met Pro	Ala Phe Arg Thr Pro	Ser Lys Ile Pro Tyr	Ser		
	365		370		375
Asp Val Asn Ile	Gly Thr Gly Val Ala	His Pro Pro Arg Trp	Thr		
	380		385		390
Ser Asp Ser Thr	Val Ala Glu Val Thr	Ser Ile Gln Leu Glu	Phe		
	395		400		405
Arg Glu Leu Ser	Arg Leu Thr Gly Asp	Lys Lys Phe Gln Glu	Ala		
	410		415		420
Val Glu Lys Val	Thr Gln His Ile His	Gly Leu Ser Gly Lys	Lys		
	425		430		435
Asp Gly Leu Val	Pro Met Phe Ile Asn	Thr His Ser Gly Leu	Phe		
	440		445		450
Thr His Leu Gly	Val Phe Thr Leu Gly	Ala Arg Ala Asp Ser	Tyr		
	455		460		465
Tyr Glu Tyr Leu	Leu Lys Gln Trp Ile	Gln Gly Gly Lys Gln	Glu		
	470		475		480
Thr Gln Leu Leu	Glu Asp Tyr Val Glu	Ala Ile Glu Gly Val	Arg		
	485		490		495
Thr His Leu Leu	Arg His Ser Glu Pro	Ser Lys Leu Thr Phe	Val		
	500		505		510
Gly Glu Leu Ala	His Gly Arg Phe Ser	Ala Lys Met Asp His	Leu		
	515		520		525
Val Cys Phe Leu	Pro Gly Thr Leu Ala	Leu Gly Val Tyr His	Gly		
	530		535		540
Leu Pro Ala Ser	His Met Glu Leu Ala	Gln Glu Leu Met Glu	Thr		
	545		550		555
Cys Tyr Gln Met	Asn Arg Gln Met Glu	Thr Gly Leu Ser Pro	Glu		
	560		565		570
Ile Val His Phe	Asn Leu Tyr Pro Gln	Pro Gly Arg Arg Asp	Val		

	575	580	585
Glu Val Lys Pro	Ala Asp Arg His Asn	Leu Leu Arg Pro	Glu Thr
	590	595	600
Val Glu Ser Leu	Phe Tyr Leu Tyr Arg	Val Thr Gly Asp Arg	Lys
	605	610	615
Tyr Gln Asp Trp	Gly Trp Glu Ile Leu	Gln Ser Phe Ser Arg	Phe
	620	625	630
Thr Arg Val Pro	Ser Gly Gly Tyr Ser	Ser Ile Asn Asn Val	Gln
	635	640	645
Asp Pro Gln Lys	Pro Glu Pro Arg Asp	Lys Met Glu Ser Phe	Phe
	650	655	660
Leu Gly Glu Thr	Leu Lys Tyr Leu Phe	Leu Leu Phe Ser Asp	Asp
	665	670	675
Pro Asn Leu Leu	Ser Leu Asp Ala Tyr	Val Phe Asn Thr Glu	Ala
	680	685	690
His Pro Leu Pro	Ile Trp Thr Pro	Ala	
	695		

<210> 13

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 13

cgccagaagg gcgtgattga cgtc 24

<210> 14

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 14

ccatccttct tcccagacag gccg 24

<210> 15

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 15

gaagcctgtg tccaggctct tcagtgagtg gtttgacctc ggtc 44

<210> 16

<211> 1524

<212> DNA

<213> Homo sapiens

<400> 16

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gcgcagctgc cctgggagga cggcaggctc gggttgctct ccggcgacct 150
ccctcggaag tgttcctct tccacctgt cgtggcctgc ctctcgctgg 200
gctttctctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250
cgggcagtca ggggacaagg gcaggagacc tcgggccctc ccgctgctg 300
ccccccagag ccgccccctg agcactggga agaagacgca tccctggggcc 350
cccaccgcct ggcagtgtg gtgcccttc gcgaacgctt cgaggagctc 400
ctgggtcttcg tgccccacat gcgcgcttc ctgagcagga agaagatccg 450
gcaccacatc tacgtgtca accaggtgga ccacttcagg ttcaaccggg 500
cagcgctcat caacgtggc ttctggaga gcagcaacag cacggactac 550
attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600
tggtttctc gaggtgggc cttccacgt ggcctccccg gagctccacc 650
ctctctacca ctacaagacc tatgtcgcg gcctctgct gctctccaag 700
cagcactacc ggctgtgcaa tgggatgtc aaccgcttct ggggctgggg 750
ccgcgaggac gacgagttct accggcgcat taaggagct gggctccagc 800
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 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens

<220>
 <221> sig_peptide
 <222> 1-42
 <223> Signal peptide.

<220>
 <221> misc_feature
 <222> 19-25, 65-71, 247-253, 285-291, 303-310
 <223> N-myristoylation site.

<220>
 <221> misc_feature
 <222> 27-31
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
 <221> TRANSMEM
 <222> 29-49
 <223> Transmembrane domain (type II).

<220>
 <221> misc_feature
 <222> 154-158
 <223> N-glycosylation site.

<220>
 <221> misc_feature
 <222> 226-233
 <223> Tyrosine kinase phosphorylation site.

<400> 17
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
 1 5 10 15
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
 20 25 30
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
 35 40 45

Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala	50	55	60
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys	65	70	75
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp	80	85	90
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe	95	100	105
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser	110	115	120
Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp	125	130	135
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu	140	145	150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp	155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala	170	175	180
Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His	185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His	200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly	215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu	230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe	245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg	260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly	275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu	290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp	305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser	320	325	

<210> 18
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 18
gcgaacgctt cgaggagtc tgg 23

<210> 19
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 19
gcagtgccggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
ttctctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
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gactggctgg tgcccagaaa gtctctttctg ccactgacgc ccccatcagg 150
gattggggcct tctttccccc ttctctttctg tgtctcctgc ctcatcggcc 200
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ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450

taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> sig_peptide

<222> 1-15

<223> Signal peptide.

<220>

<221> misc_feature

<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly
1 5 10 15

Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
20 25 30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
35 40 45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
50 55 60

Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcgcgccg 150

ggctccgggg ccgcccgccta ggccagtgcg ccgcgcctcg cccgcaggc 200

cccggcccgc agcatggagc caccggagc ccggcggggc cgcgcgcagc 250

cgcgcgtgtt gctgcgcctc tcgtgttag cgtgctcgc gctgctggga 300

ggcggcggcg gggcgggcgc cgcggcgtg ccgcgcggct gcaagcacga 350

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tgggtgtcag cagcctggaa ctgcgcagc tctgcccc agatactctg 450

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 tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
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 gaacatgatt cacaactgct ccttgattgc aagtgccta accatttcta 1150
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 gctcacgttt attcaacata ttcaaccaat attgctctgg aagcttatgt 1850

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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

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<222> 1-33
<223> Signal peptide.

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<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type II).

<400> 24

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Gly	Gly	Gly	Gly	Gly	Ala	Ala	Ala	Leu	Pro	Ala	Gly	Cys	Lys	His	35	40	45	
Asp	Gly	Arg	Pro	Arg	Gly	Ala	Gly	Arg	Ala	Ala	Gly	Ala	Ala	Glu	50	55	60	
Gly	Lys	Val	Val	Cys	Ser	Ser	Leu	Glu	Leu	Ala	Gln	Val	Leu	Pro	65	70	75	
Pro	Asp	Thr	Leu	Pro	Asn	Arg	Thr	Val	Thr	Leu	Ile	Leu	Ser	Asn	80	85	90	
Asn	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser	95	100	105	
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile	110	115	120	
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp	125	130	135	
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Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe	155	160	165	
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg	170	175	180	
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile	185	190	195	
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg	200	205	210	
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val	215	220	225	
Thr	Gly	Val	Lys	Gln	Glu	Leu	Leu	Thr	Cys	Asp	Pro	Pro	Leu	Glu	230	235	240	
Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe	245	250	255	
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp	260	265	270	
Gln	Asp	Met	Gln	Val	Leu	Trp	Tyr	Gln	Asp	Gly	Arg	Ile	Val	Glu	275	280	285	

Thr Asp Glu Ser	Gln Gly Ile Phe Val	Glu Lys Asn Met Ile His
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Asn Cys Ser Leu	Ile Ala Ser Ala Leu Thr	Ile Ser Asn Ile Gln
305		315
Ala Gly Ser Thr	Gly Asn Trp Gly Cys His	Val Gln Thr Lys Arg
320		330
Gly Asn Asn Thr	Arg Thr Val Asp Ile Val	Val Leu Glu Ser Ser
335		345
Ala Gln Tyr Cys	Pro Pro Glu Arg Val Val	Asn Asn Lys Gly Asp
350		360
Phe Arg Trp Pro	Arg Thr Leu Ala Gly Ile	Thr Ala Tyr Leu Gln
365		375
Cys Thr Arg Asn	Thr His Gly Ser Gly Ile	Tyr Pro Gly Asn Pro
380		390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg Cys	Asp Arg Gly Gly Phe
395		405
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys Gln	Tyr Ala Asn Asp Val
410		420
Thr Arg Val Leu	Tyr Met Phe Asn Gln Met	Pro Leu Asn Leu Thr
425		435
Asn Ala Val Ala	Thr Ala Arg Gln Leu Leu	Ala Tyr Thr Val Glu
440		450
Ala Ala Asn Phe	Ser Asp Lys Met Asp Val	Ile Phe Val Ala Glu
455		465
Met Ile Glu Lys	Phe Gly Arg Phe Thr Lys	Glu Glu Lys Ser Lys
470		480
Glu Leu Gly Asp	Val Met Val Asp Ile Ala	Ser Asn Ile Met Leu
485		495
Ala Asp Glu Arg	Val Leu Trp Leu Ala Gln	Arg Glu Ala Lys Ala
500		510
Cys Ser Arg Ile	Val Gln Cys Leu Gln Arg	Ile Ala Thr Tyr Arg
515		525
Leu Ala Gly Gly	Ala His Val Tyr Ser Thr	Tyr Ser Pro Asn Ile
530		540
Ala Leu Glu Ala	Tyr Val Ile Lys Ser Thr	Gly Phe Thr Gly Met
545		555
Thr Cys Thr Val	Phe Gln Lys Val Ala Ala	Ser Asp Arg Thr Gly
560		570

Leu Ser Asp Tyr Gly Arg Arg Asp Pro Glu Gly Asn Leu Asp Lys
575 580 585

Gln Leu Ser Phe Lys Cys Asn Val Ser Asn Thr Phe Ser Ser Leu
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Ala Leu Lys Val Cys Tyr Ile Leu Gln Ser Phe Lys Thr Ile Tyr
605 610 615

Ser

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 16

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<210> 17

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 27

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<210> 18

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggcct cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtcctt ttgggagaac agattatctt gactgagcaa 200
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<210> 29
 <211> 81
 <212> PRT
 <213> Homo sapiens

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 <222> 1-21
 <223> Signal peptide.

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 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
 50 55 60
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
 65 70 75
 Lys Gly Ser Gln Lys Ser
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<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

<400> 30

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tcogtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgc 150
caccaccatc acaaccacca cgacgtcacc ttccggcctg gggcccccca 200
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<210> 31
<211> 322
<212> PRT
<213> Homo sapiens

<400> 31
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35 40 45
Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
50 55 60
Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
65 70 75
Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
80 85 90
Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
95 100 105

Ala Cys Tyr Ala	Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr	110	115	120
Pro Thr Thr Tyr	Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp	125	130	135
His Ala Ile Ala	Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala	140	145	150
Tyr Ala Thr Glu	Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile	155	160	165
Thr Gly Tyr Met	Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu	170	175	180
Thr Phe Val Ala	Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn	185	190	195
Leu Tyr Gln His	Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr	200	205	210
Ala Ile Cys Phe	Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu	215	220	225
Gly Glu Cys Thr	Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu	230	235	240
Ser Gly Leu Ala	Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu	245	250	255
Val Leu Trp Pro	Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln	260	265	270
Pro Arg Arg Ser	Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr	275	280	285
Tyr Val Cys Ala	Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr	290	295	300
Ala Ile Asn Leu	Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala	305	310	315
His Leu Val Phe	Val Lys Val	320		

<210> 32

<211> 3680

<212> DNA

<213> Homo sapiens

<400> 32

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<210> 33
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 33
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 Phe Gly Thr Val Ser Cys Glu Tyr Met Leu Gly Ser Pro Leu Ser
 20 25 30
 Ser Leu Ala Gln Val Asn Leu Ser Pro Phe Ser His Pro Lys Val
 35 40 45
 His Met Asp Pro Asn Tyr Cys His Pro Ser Thr Ser Leu His Leu
 50 55 60
 Cys Ser Leu Ala Trp Ser Phe Thr Arg Leu Leu His Pro Pro Leu
 65 70 75
 Ser Pro Gly Ile Ser Gln Val Val Lys Asp His Val Thr Lys Pro
 80 85 90
 Thr Ala Met Ala Gln Gly Arg Val Ala His Leu Ile Glu Trp Lys
 95 100 105
 Gly Trp Ser Lys Pro Ser Asp Ser Pro Ala Ala Leu Glu Ser Ala
 110 115 120

Phe Ser Ser Tyr Ser Asp Leu Ser Glu Gly Glu Gln Glu Ala Arg	125	130	135
Phe Ala Ala Gly Val Ala Glu Gln Phe Ala Ile Ala Glu Ala Lys	140	145	150
Leu Arg Ala Trp Ser Ser Val Asp Gly Glu Asp Ser Thr Asp Asp	155	160	165
Ser Tyr Asp Glu Asp Phe Ala Gly Gly Met Asp Thr Asp Met Ala	170	175	180
Gly Gln Leu Pro Leu Gly Pro His Leu Gln Asp Leu Phe Thr Gly	185	190	195
His Arg Phe Ser Arg Pro Val Arg Gln Gly Ser Val Glu Pro Glu	200	205	210
Ser Asp Cys Ser Gln Thr Val Ser Pro Asp Thr Leu Cys Ser Ser	215	220	225
Leu Cys Ser Leu Glu Asp Gly Leu Leu Gly Ser Pro Ala Arg Leu	230	235	240
Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro	245	250	255
Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala	260	265	270
Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser	275	280	285
Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu	290	295	300
Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser	305	310	315
Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala	320	325	330
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<223> Synthetic oligonucleotide probe

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<210> 37
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<210> 38
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<220>
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<400> 39
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<210> 40
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<212> DNA
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<400> 40

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 ttgggtgcct taaaaactca atgagaatca tggt 2084

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 <211> 334
 <212> PRT
 <213> Homo sapiens

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 35 40 45
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 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105

Ile Ser Thr Ser	Pro Pro Leu Ile His	Ser Phe Val Ser Lys Val
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125	130	135
Ala His Pro Asn	Ala Thr Pro Ala Leu	Ser Ser Glu Asn Phe Thr
140	145	150
Trp Ser Leu Val	Asn Asp Thr Val Lys	Thr Pro Asp Asn Ser Ser
155	160	165
Ile Thr Val Ser	Ile Leu Ser Ser Glu	Pro Thr Ser Pro Ser Val
170	175	180
Thr Pro Leu Ile	Val Glu Pro Ser Gly	Trp Leu Thr Thr Asn Ser
185	190	195
Asp Ser Phe Thr	Gly Phe Thr Pro Tyr	Gln Glu Lys Thr Thr Leu
200	205	210
Gln Pro Thr Leu	Lys Phe Thr Asn Asn	Ser Lys Leu Phe Pro Asn
215	220	225
Thr Ser Asp Pro	Gln Lys Glu Asn Arg	Asn Thr Gly Ile Val Phe
230	235	240
Gly Ala Ile Leu	Gly Ala Ile Leu Gly	Val Ser Leu Leu Thr Leu
245	250	255
Val Gly Tyr Leu	Leu Cys Gly Lys Arg	Lys Thr Asp Ser Phe Ser
260	265	270
His Arg Arg Leu	Tyr Asp Asp Arg Asn	Glu Pro Val Leu Arg Leu
275	280	285
Asp Asn Ala Pro	Glu Pro Tyr Asp Val	Ser Phe Gly Asn Ser Ser
290	295	300
Tyr Tyr Asn Pro	Thr Leu Asn Asp Ser	Ala Met Pro Glu Ser Glu
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Glu Asn Ala Arg	Asp Gly Ile Pro Met	Asp Asp Ile Pro Pro Leu
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<210> 42

<211> 1594

<212> DNA

<213> Homo sapiens

<400> 42

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ccctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

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Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
			35					40						45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
			50					55						60

Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr
			65					70						75

Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys
			80					85						90

Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu
			95					100						105

Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp
			110					115						120

Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp
			125					130						135

Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr
			140					145						150

Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu
			155					160						165

Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe
			170					175						180

Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val
			185					190						195

Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn
			200					205						210

Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe
			215					220						225

Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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<210> 45
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<400> 45
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<210> 46
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<400> 46
 caggatctcc tcttgacgac tgcagc 26

<210> 47
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<400> 47
 attctcgaac cacataagtt tgaggcag 28

<210> 48
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<223> Synthetic oligonucleotide probe

<400> 48

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<210> 49

<211> 1969

<212> DNA

<213> Homo sapiens

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 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaga 1969

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 (211) 233
 (212) PRT
 (213) Homo sapiens

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 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe

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Phe	Arg	Gln	Tyr	Val	Met	Leu	Ile	Ala	Val	Val	Gly	Ser	Leu	Ala	
				95					100					105	
Phe	Leu	Leu	Met	Phe	Ile	Val	Cys	Ala	Ala	Val	Ile	Thr	Arg	Gln	
				110					115					120	
Lys	Gln	Lys	Ala	Ser	Ala	Tyr	Tyr	Pro	Ser	Ser	Phe	Pro	Lys	Lys	
				125					130					135	
Lys	Tyr	Val	Asp	Gln	Ser	Asp	Arg	Ala	Gly	Gly	Pro	Arg	Ala	Phe	
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Ser	Glu	Val	Pro	Asp	Arg	Ala	Pro	Asp	Ser	Arg	Pro	Glu	Glu	Ala	
				155					160					165	
Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
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Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
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Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
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<211> 1734

<212> DNA

<213> Homo sapiens

<400> 51

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cctggcctgc ctctgctgg cctctgcct gggcagtgg gaggctggcc 250

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 <211> 440
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly
 50 55 60
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 65 70 75
 Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly
 80 85 90
 Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala
 95 100 105
 Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val
 110 115 120
 Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val
 125 130 135
 Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile
 140 145 150
 Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro
 155 160 165
 Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser
 170 175 180
 Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln
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 215 220 225
 Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly
 230 235 240

Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser	245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly	260	265	270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser	275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser	290	295	300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305	310	315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320	325	330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335	340	345
Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn	350	355	360
Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser	365	370	375
Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly	380	385	390
Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser	395	400	405
Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser	410	415	420
Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg	425	430	435
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<211> 3580

<212> DNA

<213> Homo sapiens

<400> 53

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 <212> PRT
 <213> Homo sapiens

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 His Gly Leu Asp Asn Ala Pro Val Val Asp Gln Gln Leu Leu Tyr
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 Thr Cys Cys Pro Tyr Ile Gly Glu Leu Arg Lys Leu Leu Ala Ser
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 Trp Val Ser Gly Ser Ser Gly Arg Ser Gly Gly Phe Met Arg Lys
 80 85 90
 Ile Thr Pro Thr Thr Thr Thr Ser Leu Gly Ala Gln Pro Ser Gln
 95 100 105
 Thr Ser Gln Gly Leu Gln Ala Gln Leu Ala Gln Ala Phe Phe His
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 Asn Gln Pro Pro Ser Leu Arg Arg Thr Val Glu Phe Val Ala Glu
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 Arg Ile Gly Ser Asn Cys Val Lys His Ile Lys Ala Thr Leu Val
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Ala Asp Leu Val Arg Gln Ala Glu Ser	Leu Leu Gln Glu Gln Leu	
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Val Thr Gln Gly Glu Glu Gly Gly Asp	Pro Ala Gln Leu Leu Glu	
170	175	180
Ile Leu Cys Ser Gln Leu Cys Pro His	Gly Ala Gln Ala Leu Ala	
185	190	195
Leu Gly Arg Glu Phe Cys Gln Arg Lys	Ser Pro Gly Ala Val Arg	
200	205	210
Ala Leu Leu Pro Glu Glu Thr Pro Ala	Ala Val Leu Ser Ser Ala	
215	220	225
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230	235	240
Leu Ser Ala Asn Ile Thr Ala Leu Ile	Arg Arg Glu Val Lys Ala	
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 <212> DNA
 <213> Homo sapiens

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<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg
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Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro
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Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln
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Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val
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Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala

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 caataatccg tggcaacata tctctgtaaa aacaaacact gtaacttcta 4250
 aataaatggt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115
 <212> PRT
 <213> Homo sapiens

<400> 58
 Met Leu Arg Gly Thr Met Thr Ala Trp Arg Gly Met Arg Pro Glu
 1 5 10 15
 Val Thr Leu Ala Cys Leu Leu Leu Ala Thr Ala Gly Cys Phe Ala
 20 25 30
 Asp Leu Asn Glu Val Pro Gln Val Thr Val Gln Pro Ala Ser Thr
 35 40 45
 Val Gln Lys Pro Gly Gly Thr Val Ile Leu Gly Cys Val Val Glu
 50 55 60
 Pro Pro Arg Met Asn Val Thr Trp Arg Leu Asn Gly Lys Glu Leu
 65 70 75
 Asn Gly Ser Asp Asp Ala Leu Gly Val Leu Ile Thr His Gly Thr
 80 85 90

Leu Val Ile Thr	Ala Leu Asn Asn His	Thr Val Gly Arg Tyr Gln	95	100	105
Cys Val Ala Arg	Met Pro Ala Gly Ala	Val Ala Ser Val Pro Ala	110	115	120
Thr Val Thr Leu	Ala Asn Leu Gln Asp	Phe Lys Leu Asp Val Gln	125	130	135
His Val Ile Glu	Val Asp Glu Gly Asn	Thr Ala Val Ile Ala Cys	140	145	150
His Leu Pro Glu	Ser His Pro Lys Ala	Gln Val Arg Tyr Ser Val	155	160	165
Lys Gln Glu Trp	Leu Glu Ala Ser Arg	Gly Asn Tyr Leu Ile Met	170	175	180
Pro Ser Gly Asn	Leu Gln Ile Val Asn	Ala Ser Gln Glu Asp Glu	185	190	195
Gly Met Tyr Lys	Cys Ala Ala Tyr Asn	Pro Val Thr Gln Glu Val	200	205	210
Lys Thr Ser Gly	Ser Ser Asp Arg Leu	Arg Val Arg Arg Ser Thr	215	220	225
Ala Glu Ala Ala	Arg Ile Ile Tyr Pro	Pro Glu Ala Gln Thr Ile	230	235	240
Ile Val Thr Lys	Gly Gln Ser Leu Ile	Leu Glu Cys Val Ala Ser	245	250	255
Gly Ile Pro Pro	Pro Arg Val Thr Trp	Ala Lys Asp Gly Ser Ser	260	265	270
Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375

Leu Arg Val Leu Ser Met Gly Pro Glu Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu Asn Glu Val Gly Ser Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser Arg Pro Ser Ile Thr Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala Thr Gly Thr Pro Pro Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu Gln Met Leu Arg Gly Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser Val Gly Pro Ala Ser Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly Ala Pro Ala Glu Ala Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser Lys Thr Asp Ser Tyr Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly Ser Gly Arg Ala Pro Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys Gln Val Thr Asn Ser Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro Ala Asn Gln His Arg Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser Leu Tyr Glu Val Glu Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly Gln Thr Ala Met Val Thr Phe Arg Thr Gly Arg	560	565	570
Arg Pro Lys Pro Glu Ile Met Ala Ser Lys Glu Gln Gln Ile Gln	575	580	585
Arg Asp Asp Pro Gly Ala Ser Pro Gln Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu Ser Pro Pro Glu Ala Pro Asp Arg Pro Thr Ile	605	610	615
Ser Thr Ala Ser Glu Thr Ser Val Tyr Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly Phe Pro Ile Gln Ser Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys Val Gly Asp Trp Ile Leu Ala Thr Ser Ala Ile	650	655	660

Pro	Pro	Ser	Arg	Leu	Ser	Val	Glu	Ile	Thr	Gly	Leu	Glu	Lys	Gly		665	670	675
Thr	Ser	Tyr	Lys	Phe	Arg	Val	Arg	Ala	Leu	Asn	Met	Leu	Gly	Glu		680	685	690
Ser	Glu	Pro	Ser	Ala	Pro	Ser	Arg	Pro	Tyr	Val	Val	Ser	Gly	Tyr		695	700	705
Ser	Gly	Arg	Val	Tyr	Glu	Arg	Pro	Val	Ala	Gly	Pro	Tyr	Ile	Thr		710	715	720
Phe	Thr	Asp	Ala	Val	Asn	Glu	Thr	Thr	Ile	Met	Leu	Lys	Trp	Met		725	730	735
Tyr	Ile	Pro	Ala	Ser	Asn	Asn	Asn	Thr	Pro	Ile	His	Gly	Phe	Tyr		740	745	750
Ile	Tyr	Tyr	Arg	Pro	Thr	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Tyr	Lys		755	760	765
Lys	Asp	Met	Val	Glu	Gly	Asp	Lys	Tyr	Trp	His	Ser	Ile	Ser	His		770	775	780
Leu	Gln	Pro	Glu	Thr	Ser	Tyr	Asp	Ile	Lys	Met	Gln	Cys	Phe	Asn		785	790	795
Glu	Gly	Gly	Glu	Ser	Glu	Phe	Ser	Asn	Val	Met	Ile	Cys	Glu	Thr		800	805	810
Lys	Ala	Arg	Lys	Ser	Ser	Gly	Gln	Pro	Gly	Arg	Leu	Pro	Pro	Pro		815	820	825
Thr	Leu	Ala	Pro	Pro	Gln	Pro	Pro	Leu	Pro	Glu	Thr	Ile	Glu	Arg		830	835	840
Pro	Val	Gly	Thr	Gly	Ala	Met	Val	Ala	Arg	Ser	Ser	Asp	Leu	Pro		845	850	855
Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile		860	865	870
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln		875	880	885
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro		890	895	900
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His		905	910	915
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala		920	925	930
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala		935	940	945

Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu	950	955	960
Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His	965	970	975
Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly	980	985	990
Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro	995	1000	1005
Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys	1010	1015	1020
Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg	1025	1030	1035
Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro	1040	1045	1050
Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu	1055	1060	1065
Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp	1070	1075	1080
Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly	1085	1090	1095
Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr	1100	1105	1110
Pro Pro Leu Thr Ile	1115		

<210> 59

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 59

gggaaacaca gcagtcattg cctgc 25

<210> 60

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 60

gcacacgtag cctgtcgtg gaggc 24

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 61
caccoccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62
<211> 1661
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 678
<223> unknown base

<400> 62
cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccat 50
cgctctctcc tcccaggctc ccggggccga ccccccggca acatgcagcc 100
cacggggccg gaggggtccc gcgcgctcag ccggcgggtat ctgcggcgtc 150
tctctctctt gctactgctg ctgctgctgc ggcagccctt aacccggcgg 200
gagaccacgc cggggcgcgc cagagccctc tccacgttgg gctcccccag 250
cctcttcacc acgcggggtg tcccacgcgc cctcactacc ccagggtctc 300
ctacgcacgg caccoccaaa accctggacc ttccggggtcg ccgcacagcc 350
ctgatgggga gtttccact cgtggacggc cacaatgacc tgcccaggt 400
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500
gcccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
cgtgcgcctc gccctggagc agattgacct cattcacgc atgtgtgct 600
cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700
cagcctctct gtgctgcgca gtttctatgt gctgggggtg cgtacctga 750
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800
agacaccaca tgtacaccaa cgtcagcgga ttgacaagct ttggtgagaa 850

agtagtagag gagttgaacc gcctgggcat gatgatagat ttgtcctatg 900
 catcggacac cttgataaga agggctcctgg aagtgtctca ggctcctgtg 950
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtga 1050
 cactgtccat ggggggtgctg cagtgcacc tgettgttaa cgtgtccact 1100
 gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150
 cgggattggt ggaaattatg acgggaactgg ccgggttcct caggggctgg 1200
 aggatgtgtc cacataccca gtcctgatag aggagttgct gagtcgtasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggaggctga gtttccatat gggcaactga gcacatcctg ccactcccac 1400
 ctogtgcttc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaccaat cgggtccctt ggaggtcttc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgetgacaca gtcgggtccc gcagaggtca ctgtggcaaa gcttcacaaa 1600
 gccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgtta 1650
 cccatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<210>
 <211> unsure
 <212> 196, 386
 <213> unknown amino acid

<400> 63
 Met Gln Pro Thr Gly Arg Glu Gly Ser Arg Ala Leu Ser Arg Arg
 1 5 10 15
 Tyr Leu Arg Arg Leu Leu Leu Leu Leu Leu Leu Leu Arg
 20 25 30
 Gln Pro Val Thr Arg Ala Glu Thr Thr Pro Gly Ala Pro Arg Ala
 35 40 45
 Leu Ser Thr Leu Gly Ser Pro Ser Leu Phe Thr Thr Pro Gly Val
 50 55 60

Pro Ser Ala Leu Thr Thr Pro Gly Leu Thr Thr Pro Gly Thr Pro	65	70	75
Lys Thr Leu Asp Leu Arg Gly Arg Ala Gln Ala Leu Met Arg Ser	80	85	90
Phe Pro Leu Val Asp Gly His Asn Asp Leu Pro Gln Val Leu Arg	95	100	105
Gln Arg Tyr Lys Asn Val Leu Gln Asp Val Asn Leu Arg Asn Phe	110	115	120
Ser His Gly Gln Thr Ser Leu Asp Arg Leu Arg Asp Gly Leu Val	125	130	135
Gly Ala Gln Phe Trp Ser Ala Ser Val Ser Cys Gln Ser Gln Asp	140	145	150
Gln Thr Ala Val Arg Leu Ala Leu Glu Gln Ile Asp Leu Ile His	155	160	165
Arg Met Cys Ala Ser Tyr Ser Glu Leu Glu Leu Val Thr Ser Ala	170	175	180
Glu Gly Leu Asn Ser Ser Gln Lys Leu Ala Cys Leu Ile Gly Val	185	190	195
Xaa Gly Gly His Ser Leu Asp Ser Ser Leu Ser Val Leu Arg Ser	200	205	210
Phe Tyr Val Leu Gly Val Arg Tyr Leu Thr Leu Thr Phe Thr Cys	215	220	225
Ser Thr Pro Trp Ala Glu Ser Ser Thr Lys Phe Arg His His Met	230	235	240
Tyr Thr Asn Val Ser Gly Leu Thr Ser Phe Gly Glu Lys Val Val	245	250	255
Glu Glu Leu Asn Arg Leu Gly Met Met Ile Asp Leu Ser Tyr Ala	260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro	275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu	290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly	305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu	320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg	335	340	345

Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
	350	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
	365	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
	380	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
	395	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
	410	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
	425	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
	440	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
	455	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
	470	480
Thr Phe Thr Gln Trp Leu Cys		
	485	

<210> 64
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 64
 cttcacctg cagtacacca tgggc 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 65
 gtcacacaca gctctggcag ctgag 25

<210> 66
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgcctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacaccccaca gatccctcta tgaactgcaat gtgagggtgtc cggcctttgct 100
ggcccagcaaa gcttgataag catgaagctc ttatcttttg tggtgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt totgaagata 200
tcgggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtgggtgga 300
gcccattgcaa gtgcttggtc atgaactgga ggcttaactgc ctgctgtgag 350
agtgcaggtc caggagagcg agcaccacca ccatcaaggt catcattgtc 400
atctactgtt ccgtggtggg tgcctgtttg ctctacatgg ccttctctgat 450
gttgggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acattgagga ggagaatgag gatgctcgtc ctatggcagc agctgctgca 550
tcctctgggg gaccccgagc aaacacagtc ctggagcgtg tgggaaggtgc 600
ccagcagcgg tgggaagctgc aggtgcagga gcagcgggaag acagtctctg 650
atgggcacaa gatgctcagc tagatgggtt ggtgtggttg ggtcaaggcc 700
ccaacacccat ggtgcccagc ttccaggctg gacaaaagcag ggggctaact 750
ctcccttccc tgggttccag tcttcccttt aaaagcctgt ggcatttttc 800
ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850
aagaggggatg tggctcttga tctctgttgt cttcttgggt ctttggggtt 900
gaaggggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
ctcaggagtg gatgcatct gtctctctct gctccactct tgcgccttc 1000
cagctctgag tcttgggaat gttgttacc ttggaagata aagctgggtc 1050
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
gttctcttct gcagtgggtc ttatcaccac ctccctccca gcccgggcgc 1150

ctcagcccca gccccagctc cagccctgag gacagctctg atgggagagc 1200
 tgggccccct gagcccaactg ggtcttcagg gtgcactgga agctgggtgtt 1250
 cgctgtcccc tgtgcacttc tcgcactggg gcatggagtg cccatgcata 1300
 ctctgtctgc ggccccctca cctgcacttg aggggtcttg gcagtcacctc 1350
 ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400
 gactcgaggc tgagcgtgga tctgaacacc acagccctg tacttgggtt 1450
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 ttttatttct ctca 1564

<210> 68
 <211> 183
 <212> PFT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60
 Pro Met Pro Val Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu
 65 70 75
 Cys Glu Cys Arg Tyr Glu Glu Arg Ser Thr Thr Thr Ile Lys Val
 80 85 90
 Ile Ile Val Ile Tyr Leu Ser Val Val Gly Ala Leu Leu Leu Tyr
 95 100 105
 Met Ala Phe Leu Met Leu Val Asp Pro Leu Ile Arg Lys Pro Asp
 110 115 120
 Ala Tyr Thr Glu Gln Leu His Asn Glu Glu Glu Asn Glu Asp Ala
 125 130 135
 Arg Ser Met Ala Ala Ala Ala Ala Ser Leu Gly Gly Pro Arg Ala
 140 145 150
 Asn Thr Val Leu Glu Arg Val Glu Gly Ala Gln Gln Arg Trp Lys
 155 160 165

Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe Asp Arg His Lys
170 175 180

Met Leu Ser

<210> 69
<211> 3170
<212> DNA
<213> Homo sapiens

<400> 69
agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
agttcatagg gtcttgggtc cccgaaccag gaagggttga gggaacacaa 100
tctgcaagcc ccgcgaccc aagtgagggg ccccggttg gggctctccc 150
tccttttgca tccccacccc tcggggcttt gcgtcttctt ggggaccccc 200
tcgcccggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
tcgcgggcca aactcaactc catcaagtc tctctgggcg gggagacgcc 350
tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
ggcgagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450
gataaggagt gtgaagttgg gaggtattgc cacagtcacc accaaggatc 500
atcggcctgc atggtgtgtc ggagaaaaaa gaagcgctgc caccgagatg 550
gcatgtgctg cccagtagc cgctgcaata atggcatctg tatcccagtt 600
actgaaagca tcttaacccc tcacatcccc gctctggatg gtactcggca 650
cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750
gacccctgcc tacgatcacc agactgcatt gaagggtttt gctgtgctcg 800
tcattttctg accaaaatct gcaaaccagt gctccatcag ggggaagtct 850
gtaccaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950
ctctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050
catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100

gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150
 aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200
 caactgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250
 agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300
 aagagtttag gttgtgctgg aggagaggtt tocttcagat tgctgattgc 1350
 ttatacaaat aacctacatg ccagatttct attcaacgtt agagtttaac 1400
 aaaatactcc tagaataact tgttatacaa taggtttctaa aaataaaatt 1450
 gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500
 taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggg 1550
 agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600
 cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650
 ccacaaatac ttttttttca aaattttagt ttacctgta attaataaga 1700
 actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750
 atctctcttt atcttatgtg attcctgctc tgaatgcatt atattttcca 1800
 aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850
 ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900
 gctaacagag agatcattat ttcttaaaga ttggccttaa cctatatattt 1950
 gatagaatta gattggtaaa tacatgtatt catacatact ctgtggtaat 2000
 agagacttaa gctggatctg tactgcactg gagtaagcaa gaaaattggg 2050
 aaaacttttt cgtttgttca ggttttggca acacatagat catatgtctg 2100
 aggcacaagt tggctgttca tctttgaaac caggggatgc acagtctaaa 2150
 tgaatatctg catgggattt gctatcataa tatttactat gcagatgaat 2200
 tcagtgtgag gtctgtgtc cgtactatcc tcaaattatt tattttatag 2250
 tgctgagatc ctcaaataat ctcaatttca ggagggttca caaatgtac 2300
 tctgaagta gacagagtag tgagggttca ttgocctcta taagcttctg 2350
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 ctttattgcc aaagggctag ttccggtttt ctgcagccat tgcgggttaa 2450
 aaatataagt aggataactt gtaaaacctg catattgcta atctatagac 2500
 accacagttt ctaaattctt tgaaaccact ttactacttt ttttaaactt 2550

aactcagttc taaatacttt gtctggagca caaaacaata aaaggttata 2600
ttatagtcgt gactttaaac tttttagac cacaattcac tttttagttt 2650
tcttttactt aaatcccatc tgcagttctca aatttaagtt ctcccagtag 2700
agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750
tatttactaa gatgattaag acttacattt tctgcacagg tctgcaaaaa 2800
caaaaattat aaactagtcc atccaagaac caaagtttgt ataaacaggt 2850
tgctataagc ttgtgaaatg aaaatggaac atttcaatca aacatttctt 2900
atataacaat tattatattt acaatttggt ttctgcaata tttttcttat 2950
gtccaccctt ttaaaaatta ttatttgaag taattttatt acaggaaatg 3000
ttaatgagat gtattttctt atagagatat ttcttacaga aagctttgta 3050
gcagaatata tttgcagcta ttgactttgt aatttaggaa aaatgtataa 3100
taagataaaa tctattaaat ttttctctc taaaaactga aaaaaaaaaa 3150
aaaaaaaaa aaaaaaaaaa 3170

<210> 70
<211> 259
<212> PRT
<213> Homo sapiens

<400> 70
Met Ala Ala Leu Met Arg Ser Lys Asp Ser Ser Cys Cys Leu Leu
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Leu Leu Ala Ala Val Leu Met Val Glu Ser Ser Gln Ile Gly Ser
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Ser Arg Ala Lys Leu Asn Ser Ile Lys Ser Ser Leu Gly Gly Glu
35 40 45
Thr Pro Gly Gln Ala Ala Asn Arg Ser Ala Gly Met Tyr Gln Gly
50 55 60
Leu Ala Phe Gly Gly Ser Lys Lys Gly Lys Asn Leu Gly Gln Ala
65 70 75
Tyr Pro Cys Ser Ser Asp Lys Glu Cys Glu Val Gly Arg Tyr Cys
80 85 90
His Ser Pro His Gln Gly Ser Ser Ala Cys Met Val Cys Arg Arg
95 100 105
Lys Lys Lys Arg Cys His Arg Asp Gly Met Cys Cys Pro Ser Thr
110 115 120

Arg Cys Asn Asn Gly Ile Cys Ile Pro Val Thr Glu Ser Ile Leu	125	130	135
Thr Pro His Ile Pro Ala Leu Asp Gly Thr Arg His Arg Asp Arg	140	145	150
Asn His Gly His Tyr Ser Asn His Asp Leu Gly Trp Gln Asn Leu	155	160	165
Gly Arg Pro His Thr Lys Met Ser His Ile Lys Gly His Glu Gly	170	175	180
Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly Phe Cys Cys	185	190	195
Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu His Gln	200	205	210
Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly Leu	215	220	225
Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	230	235	240
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val	245	250	255

Cys Gln Lys Ile

<210> 71

<211> 1809

<212> DNA

<213> Homo sapiens

<400> 71

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acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150

cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatattt catgtagtat tttctaagtt 250

atatttttagt aattcatatg ttttagatta taggttttaa catacttgtg 300

aaaatacttg atgtgtttta aagccttggg cagaaattct gtattgttga 350

ggatttggtc ttttatcccc cttttaaagt catccgtcct tggctcagga 400

tttgagagc ttgcaccacc aaaaatggca aacatcacca gctccagat 450

tttgaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500

gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550

ctcaagcccc caacatoccca gtccctcagtc ctcagtcato ttgacttcaa 600
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 agcaccagag ccaggcagtc actgttcttc ctccctgggtt ggagtccttt 700
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 tgtctgtcca ccagccacag cccaaacaca tcaaacttgc taagcggcgg 850
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 aatcagattc ccacagctt gtattcgaag tctttaagtg agcctttgaa 1050
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 gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750
 gaggcacaag aatcgcttga gccagcttgg gctacaaagt gagactccgt 1800
 ctgaaaaga 1809

<210> 72

<211> 363

<212> PRT

<213> Homo sapiens

<400> 72

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Cys	Ser	Phe	Ile	Pro	Leu	Leu	Lys	Ser	Ser	Val	Leu	Gly	Ser	Gly
				20					25					30
Phe	Gly	Glu	Leu	Ala	Pro	Pro	Lys	Met	Ala	Asn	Ile	Thr	Ser	Ser
				35					40					45
Gln	Ile	Leu	Asp	Gln	Leu	Lys	Ala	Pro	Ser	Leu	Gly	Gln	Phe	Thr
				50					55					60
Thr	Thr	Pro	Ser	Thr	Gln	Gln	Asn	Ser	Thr	Ser	His	Pro	Thr	Thr
				65					70					75
Thr	Thr	Ser	Trp	Asp	Leu	Lys	Pro	Pro	Thr	Ser	Gln	Ser	Ser	Val
				80					85					90
Leu	Ser	His	Leu	Asp	Phe	Lys	Ser	Gln	Pro	Glu	Pro	Ser	Pro	Val
				95					100					105
Leu	Ser	Gln	Leu	Ser	Gln	Arg	Gln	Gln	His	Gln	Ser	Gln	Ala	Val
				110					115					120
Thr	Val	Pro	Pro	Pro	Gly	Leu	Glu	Ser	Phe	Pro	Ser	Gln	Ala	Lys
				125					130					135
Leu	Arg	Glu	Ser	Thr	Pro	Gly	Asp	Ser	Pro	Ser	Thr	Val	Asn	Lys
				140					145					150
Leu	Leu	Gln	Leu	Pro	Ser	Thr	Thr	Ile	Glu	Asn	Ile	Ser	Val	Ser
				155					160					165
Val	His	Gln	Pro	Gln	Pro	Lys	His	Ile	Lys	Leu	Ala	Lys	Arg	Arg
				170					175					180
Ile	Pro	Pro	Ala	Ser	Lys	Ile	Pro	Ala	Ser	Ala	Val	Glu	Met	Pro
				185					190					195
Gly	Ser	Ala	Asp	Val	Thr	Gly	Leu	Asn	Val	Gln	Phe	Gly	Ala	Leu
				200					205					210
Glu	Phe	Gly	Ser	Glu	Pro	Ser	Leu	Ser	Glu	Phe	Gly	Ser	Ala	Pro
				215					220					225
Ser	Ser	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Ser	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser

	275		280		285
Ser Ser Tyr Asp Gln Ser Ser Val His Asn Arg Ile Pro Tyr Gln					
	290		295		300
Ser Pro Val Ser Ser Ser Glu Ser Ala Pro Gly Thr Ile Met Asn					
	305		310		315
Gly His Gly Gly Gly Arg Ser Gln Gln Thr Leu Asp Ser Lys Tyr					
	320		325		330
Ser Ser Lys Leu Leu Leu Ser Trp Leu Val Pro Thr Lys Gln Arg					
	335		340		345
Lys Arg Ile Ala His Val Met Trp Lys Thr Pro Val Gly Gln Trp					
	350		355		360
Leu Ile Arg					

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 74
 tggtaaaactg gcccaaactc gg 22

<210> 75
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 75
 ttaaagtcac ccgtccttgg ctcaggattt ggagagcttg caccaccaa 50

<210> 76
 <211> 1989
 <212> DNA
 <213> Homo sapiens

<400> 76

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tjcaactcagc ggtggaggag acggacggg ggtgtacac ctgcaacctg 150
caacataact actgccacct ctacgagagc ctggcctgc goctggagg 200
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ccactctcag cccccacat ttgcatctgc tggaggacct gccaccatca 1950
caataagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77
<211> 341
<212> PRT
<213> Homo sapiens

<400> 77
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Gln Ser Ser Ala Val Leu Leu His Ser Ala Val Glu Glu Thr Asp
20 25 30
Ala Gly Leu Tyr Thr Cys Asn Leu His His His Tyr Cys His Leu
35 40 45
Tyr Glu Ser Leu Ala Val Arg Leu Glu Val Thr Asp Gly Pro Pro
50 55 60
Ala Thr Pro Ala Tyr Trp Asp Gly Glu Lys Glu Val Leu Ala Val
65 70 75
Ala Arg Gly Ala Pro Ala Leu Leu Thr Cys Val Asn Arg Gly His
80 85 90
Val Trp Thr Asp Arg His Val Glu Glu Ala Gln Gln Val Val His
95 100 105
Trp Asp Arg Gln Pro Pro Gly Val Pro His Asp Arg Ala Asp Arg
110 115 120
Leu Leu Asp Leu Tyr Ala Ser Gly Glu Arg Arg Ala Tyr Gly Pro
125 130 135

Leu Phe Leu Arg Asp Arg Val Ala Val Gly Ala Asp Ala Phe Glu	140	145	150
Arg Gly Asp Phe Ser Leu Arg Ile Glu Pro Leu Glu Val Ala Asp	155	160	165
Glu Gly Thr Tyr Ser Cys His Leu His His His Tyr Cys Gly Leu	170	175	180
His Glu Arg Arg Val Phe His Leu Thr Val Ala Glu Pro His Ala	185	190	195
Glu Pro Pro Pro Arg Gly Ser Pro Gly Asn Gly Ser Ser His Ser	200	205	210
Gly Ala Pro Gly Pro Asp Pro Thr Leu Ala Arg Gly His Asn Val	215	220	225
Ile Asn Val Ile Val Pro Glu Ser Arg Ala His Phe Phe Gln Gln	230	235	240
Leu Gly Tyr Val Leu Ala Thr Leu Leu Leu Phe Ile Leu Leu Leu	245	250	255
Val Thr Val Leu Leu Ala Ala Arg Arg Arg Arg Gly Gly Tyr Glu	260	265	270
Tyr Ser Asp Gln Lys Ser Gly Lys Ser Lys Gly Lys Asp Val Asn	275	280	285
Leu Ala Glu Phe Ala Val Ala Ala Gly Asp Gln Met Leu Tyr Arg	290	295	300
Ser Glu Asp Ile Gln Leu Asp Tyr Lys Asn Asn Ile Leu Lys Glu	305	310	315
Arg Ala Glu Leu Ala His Ser Pro Leu Pro Ala Lys Tyr Ile Asp	320	325	330
Leu Asp Lys Gly Phe Arg Lys Glu Asn Cys Lys	335	340	

<210> 78

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 78

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cagtctccga gctgaccagg aggcaactgt tgagaagctg ctggaccgcc 150

cgccccctgg cctgcagagg cccgaggacc gttctgtgg cacatacatc 200

atcttcttca gcctgggcat tggcagtcta ctgccatgga acttctttat 250
 cactgccaaag gagtactgga tgttcaaact ccgcaactcc tccagcccag 300
 ccaccgggga ggaccctgag ggctcagaca tctgaacta ctttgagagc 350
 taccttgccg ttgcctccac cgtgccctcc atgctgtgcc tgggtggccaa 400
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 gacacttctt cctggaccgg tggttttttt gcggtcacca ttgtctgcat 550
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 tgaagatgag aagagagtgc aggagggtg ggggccatg aggaaaggcc 1550
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 ggctggggtt ttcaaaaaaa gagggatcct catgacctgg tgggtctatgg 2150
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 gccattgggt caagggcgta ataaatactt gcgtattcaa aaa 2243

<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	
Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120	
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135	

Leu Ala Ser Leu Thr Val Ile Leu Ala Ile Phe Met Val Ile Thr	140	145	150
Ala Leu Val Lys Val Asp Thr Ser Ser Trp Thr Arg Gly Phe Phe	155	160	165
Ala Val Thr Ile Val Cys Met Val Ile Leu Ser Gly Ala Ser Thr	170	175	180
Val Phe Ser Ser Ser Ile Tyr Gly Met Thr Gly Ser Phe Pro Met	185	190	195
Arg Asn Ser Gln Ala Leu Ile Ser Gly Gly Ala Met Gly Gly Thr	200	205	210
Val Ser Ala Val Ala Ser Leu Val Asp Leu Ala Ala Ser Ser Asp	215	220	225
Val Arg Asn Ser Ala Leu Ala Phe Phe Leu Thr Ala Thr Ile Phe	230	235	240
Leu Val Leu Cys Met Gly Leu Tyr Leu Leu Leu Ser Arg Leu Glu	245	250	255
Tyr Ala Arg Tyr Tyr Met Arg Pro Val Leu Ala Ala His Val Phe	260	265	270
Ser Gly Glu Glu Glu Leu Pro Gln Asp Ser Leu Ser Ala Pro Ser	275	280	285
Val Ala Ser Arg Phe Ile Asp Ser His Thr Pro Pro Leu Arg Pro	290	295	300
Ile Leu Lys Lys Thr Ala Ser Leu Gly Phe Cys Val Thr Tyr Val	305	310	315
Phe Phe Ile Thr Ser Leu Ile Tyr Pro Ala Val Cys Thr Asn Ile	320	325	330
Glu Ser Leu Asn Lys Gly Ser Gly Ser Leu Trp Thr Thr Lys Phe	335	340	345
Phe Ile Pro Leu Thr Thr Phe Leu Leu Tyr Asn Phe Ala Asp Leu	350	355	360
Cys Gly Arg Gln Leu Thr Ala Trp Ile Gln Val Pro Gly Pro Asn	365	370	375
Ser Lys Ala Leu Pro Gly Phe Val Leu Leu Arg Thr Cys Leu Ile	380	385	390
Pro Leu Phe Val Leu Cys Asn Tyr Gln Pro Arg Val His Leu Lys	395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr Pro Ala Leu Leu Ser Ser	410	415	420

Leu Leu Gly Leu Ser Asn Gly Tyr Leu Ser Thr Leu Ala Leu Leu
 425 430 435
 Tyr Gly Pro Lys Ile Val Pro Arg Glu Leu Ala Glu Ala Thr Gly
 440 445 450
 Val Val Met Ser Phe Tyr Val Cys Leu Gly Leu Thr Leu Gly Ser
 455 460 465
 Ala Cys Ser Thr Leu Leu Val His Leu Ile
 470 475

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 80
 ttttgaggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 81
 cgttaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 82
 taaggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844
 <212> DNA
 <213> Homo sapiens

<400> 83
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 tctctgtctt cgtcccccac ctctcagcc tgggtggcctc ccaggactgg 150

aaggctgaac gcagccaaga ccccttcgag aaatgcatgc aggatcctga 200
ctatgagcag ctgctcaagg tggtagcctg ggggctcaat cggaccctga 250
agccccagag ggtgattgtg gttggcgctg gtgtggccgg gctgggtggc 300
gccaaaggtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
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ggattgggga gctgggagcc atgcgcacgc ccagctctca caggatcctc 450
cacaagctct gccagggcct ggggctcaac ctgaccaagt tcaccagta 500
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> FRT
 <213> Homo sapiens

<400> 84
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 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165
 Leu Gly Tyr Ala Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu
 170 175 180
 Asp Ile Tyr Gln Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys
 185 190 195

Ala Leu Gly Cys Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu	455	460	465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly	470	475	480

Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys	485	490	495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro	500	505	510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu	515	520	525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp	530	535	540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu	545	550	555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His	560	565	

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 <212> DNA
 <213> Homo sapiens

<400> 85
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 gaactcagag ccgggaagcc cccattcact agaagcactg agagatggcg 200
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 ccgtcttacc tttctctgac ctgaacaatc agtctgtggg aattgaggga 400
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 gacctgagcg tcctctgctt caccagtggg accacaggtg accccaaagg 1050
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25				30	

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile					
				50					55					60					
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys					
				65					70					75					
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg					
				80					85					90					
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val					
				95					100					105					
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn					
				110					115					120					
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu					
				125					130					135					
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu					
				140					145					150					
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys					
				155					160					165					
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His					
				170					175					180					
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala					
				185					190					195					
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr					
				200					205					210					
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu					
				215					220					225					
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile					
				230					235					240					
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu					
				245					250					255					
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro					
				260					265					270					
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu					
				275					280					285					
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe					
				290					295					300					
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys					
				305					310					315					
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr					

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His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
335	340	345
Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
470	475	480
Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
485	490	495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
500	505	510
Thr Leu Pro Gly Asp Trp Thr Ser Gly	His Val Gly Val Pro Leu	
515	520	525
Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
530	535	540
Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
545	550	555
Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
560	565	570
Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
575	580	585
Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	

605	610	615
Asn Ile Tyr Asn Arg Ser Gln Pro Val	Leu Gln Ile Phe Val	His
620	625	630
Gly Glu Ser Leu Arg Ser Ser Leu Val	Gly Val Val Val Pro	Asp
635	640	645
Thr Asp Val Leu Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys	Gly
650	655	660
Ser Phe Glu Glu Leu Cys Gln Asn Gln	Val Val Arg Glu Ala	Ile
665	670	675
Leu Glu Asp Leu Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys	Thr
680	685	690
Phe Glu Gln Val Lys Ala Ile Phe Leu	His Pro Glu Pro Phe	Ser
695	700	705
Ile Glu Asn Gly Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg	Gly
710	715	720
Glu Leu Ser Lys Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr	Glu
725	730	735
His Ile Gln Asp		

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 <111> 660
 <112> PFT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105

Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu	110	115	120
Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val	125	130	135
Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390

Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe		395	400	405
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr		410	415	420
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu		425	430	435
Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly		440	445	450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys		455	460	465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg		470	475	480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val		485	490	495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly		500	505	510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val		515	520	525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala		530	535	540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu		545	550	555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr		560	565	570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp		575	580	585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp		590	595	600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe		605	610	615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro		620	625	630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu		635	640	645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr		650	655	660

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<211> 25

<212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

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 <213> Artificial Sequence

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 <400> 90
 cctcaaccag gccacgggcc ac 22

 <210> 91
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 <400> 91
 cccaggcaga gatgcagtac aggc 24

 <210> 92
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 <212> DNA
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 <400> 92
 cctccagtag gtggatggat tggctc 26

 <210> 93
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 <212> DNA
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 <223> Synthetic oligonucleotide probe

 <400> 93
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 <210> 94
 <211> 3037
 <212> DNA
 <213> Homo sapiens

<400> 94

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<210> 95
 <211> 307
 <212> PRT
 <213> Homo sapiens

<400> 95
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 20 25 30
 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
 35 40 45
 Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
 50 55 60
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
 65 70 75
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
 80 85 90
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
 95 100 105
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
 110 115 120
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
 125 130 135
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
 140 145 150
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
 155 160 165
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
 170 175 180
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
 185 190 195
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
 200 205 210

Leu	Leu	Val	Phe	Ala	Leu	Ala	Ala	Pro	Val	Met	Ser	Met	Val	Thr	215	220	225
Tyr	Leu	Gly	Leu	Ser	Lys	Ser	Ser	Lys	Glu	Ala	Leu	Ser	Glu	Val	230	235	240
Asn	Ala	Thr	Gly	Val	Ala	Met	Leu	Phe	Ser	Ala	Gly	Thr	Phe	Leu	245	250	255
Tyr	Val	Ala	Thr	Val	His	Val	Leu	Pro	Glu	Val	Gly	Gly	Ile	Gly	260	265	270
His	Ser	His	Lys	Pro	Asp	Ala	Thr	Gly	Gly	Arg	Gly	Leu	Ser	Arg	275	280	285
Leu	Glu	Val	Ala	Ala	Leu	Val	Leu	Gly	Cys	Leu	Ile	Pro	Leu	Ile	290	295	300
Leu	Ser	Val	Gly	His	Gln	His									305		

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 96
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<210> 97
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 <212> DNA
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<220>
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<400> 97
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<210> 98
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 <212> DNA
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<220>
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<210> 99
 <211> 1429

<212> DNA

<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg ggcgtcgcag catgaagtcg 150
ccgcccctcg tgctggcgcc cctgggtggc tgcctcatcg tcttgggctt 200
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gaaatgtact aaataaaatg tacatctga 1429

<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Leu	Val	Leu	Ala	Ala	Leu	Val	Ala	Cys	Ile	Ile	Val	Leu	Gly	Phe
			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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230	235	240
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245	250	255
Asn Glu Ile Gln Val Val Asn Glu Glu	Pro Gln Arg Asp Arg Leu	
260	265	270
Pro Gln Glu Pro Gly Arg Glu Gln Val	Val Glu Asp Arg Pro Val	
275	280	285
Gly Gly Arg Gly Phe Gly Gly Ala Gly	Glu Leu Gly Gln Thr Pro	
290	295	300
Gln Val Gln Ala Ala Leu Ser Val Ser	Gln Glu Asn Pro Glu Met	
305	310	315
Glu Gly Pro Glu Arg Asp Gln Leu Val	Ile Pro Asp Gly Gln Glu	
320	325	330
Glu Glu Gln Glu Ala Ala Gly Glu Gly	Arg Asn Gln Gln Lys Leu	
335	340	345
Arg Gly Glu Asp Asp Tyr Asn Met Asp	Glu Asn Glu Ala Glu Ser	
350	355	360
Glu Thr Asp Lys Gln Ala Ala Leu Ala	Gly Asn Asp Arg Asn Ile	
365	370	375
Asp Val Phe Asn Val Glu Asp Gln Lys	Arg Asp Thr Ile Asn Leu	
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395	400	

<210> 101

<211> 3671

<212> DNA

<213> Homo sapiens

<400> 101

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<210> 102
 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102

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Leu	Phe	Tyr	Ala	Gly	Ile	Ala	Leu	Phe	Thr	Ser	Gly	Phe	Leu	Leu	20	25	30	
Thr	Arg	Leu	Glu	Leu	Thr	Asn	His	Ser	Ser	Cys	Gln	Glu	Pro	Pro	35	40	45	
Gly	Pro	Gly	Ser	Leu	Pro	Trp	Gly	Ser	Gln	Gly	Lys	Pro	Gly	Ala	50	55	60	
Cys	Trp	Met	Ala	Ser	Arg	Phe	Ser	Arg	Val	Val	Leu	Val	Leu	Ile	65	70	75	
Asp	Ala	Leu	Arg	Phe	Asp	Phe	Ala	Gln	Pro	Gln	His	Ser	His	Val	80	85	90	
Pro	Arg	Glu	Pro	Pro	Val	Ser	Leu	Pro	Phe	Leu	Gly	Lys	Leu	Ser	95	100	105	
Ser	Leu	Gln	Arg	Ile	Leu	Glu	Ile	Gln	Pro	His	His	Ala	Arg	Leu	110	115	120	
Tyr	Arg	Ser	Gln	Val	Asp	Pro	Pro	Thr	Thr	Thr	Met	Gln	Arg	Leu	125	130	135	
Lys	Ala	Leu	Thr	Thr	Gly	Ser	Leu	Pro	Thr	Phe	Ile	Asp	Ala	Gly	140	145	150	
Ser	Asn	Phe	Ala	Ser	His	Ala	Ile	Val	Glu	Asp	Asn	Leu	Ile	Lys	155	160	165	

Gln	Leu	Thr	Ser	Ala	Gly	Arg	Arg	Val	Val	Phe	Met	Gly	Asp	Asp	
				170					175					180	
Thr	Trp	Lys	Asp	Leu	Phe	Pro	Gly	Ala	Phe	Ser	Lys	Ala	Phe	Phe	
				185					190					195	
Phe	Pro	Ser	Phe	Asn	Val	Arg	Asp	Leu	Asp	Thr	Val	Asp	Asn	Gly	
				200					205					210	
Ile	Leu	Glu	His	Leu	Tyr	Pro	Thr	Met	Asp	Ser	Gly	Glu	Trp	Asp	
				215					220					225	
Val	Leu	Ile	Ala	His	Phe	Leu	Gly	Val	Asp	His	Cys	Gly	His	Lys	
				230					235					240	
His	Gly	Pro	His	His	Pro	Glu	Met	Ala	Lys	Lys	Leu	Ser	Gln	Met	
				245					250					255	
Asp	Gln	Val	Ile	Gln	Gly	Leu	Val	Glu	Arg	Leu	Glu	Asn	Asp	Thr	
				260					265					270	
Leu	Leu	Val	Val	Ala	Gly	Asp	His	Gly	Met	Thr	Thr	Asn	Gly	Asp	
				275					280					285	
His	Gly	Gly	Asp	Ser	Glu	Leu	Glu	Val	Ser	Ala	Ala	Leu	Phe	Leu	
				290					295					300	
Tyr	Ser	Pro	Thr	Ala	Val	Phe	Pro	Ser	Thr	Pro	Pro	Glu	Glu	Pro	
				305					310					315	
Glu	Val	Ile	Pro	Gln	Val	Ser	Leu	Val	Pro	Thr	Leu	Ala	Leu	Leu	
				320					325					330	
Leu	Gly	Leu	Pro	Ile	Pro	Phe	Gly	Asn	Ile	Gly	Glu	Val	Met	Ala	
				335					340					345	
Glu	Leu	Phe	Ser	Gly	Gly	Glu	Asp	Ser	Gln	Pro	His	Ser	Ser	Ala	
				350					355					360	
Leu	Ala	Gln	Ala	Ser	Ala	Leu	His	Leu	Asn	Ala	Gln	Gln	Val	Ser	
				365					370					375	
Arg	Phe	Leu	His	Thr	Tyr	Ser	Ala	Ala	Thr	Gln	Asp	Leu	Gln	Ala	
				380					385					390	
Lys	Glu	Leu	His	Gln	Leu	Gln	Asn	Leu	Phe	Ser	Lys	Ala	Ser	Ala	
				395					400					405	
Asp	Tyr	Gln	Trp	Leu	Leu	Gln	Ser	Pro	Lys	Gly	Ala	Glu	Ala	Thr	
				410					415					420	
Leu	Pro	Thr	Val	Ile	Ala	Glu	Leu	Gln	Gln	Phe	Leu	Arg	Gly	Ala	
				425					430					435	
Arg	Ala	Met	Cys	Ile	Glu	Ser	Trp	Ala	Arg	Phe	Ser	Leu	Val	Arg	
				440					445					450	

Met	Ala	Gly	Gly	Thr	Ala	Leu	Leu	Ala	Ala	Ser	Cys	Phe	Ile	Cys	
				455					460					465	
Leu	Leu	Ala	Ser	Gln	Trp	Ala	Ile	Ser	Pro	Gly	Phe	Pro	Phe	Cys	
				470					475					480	
Pro	Leu	Leu	Leu	Thr	Pro	Val	Ala	Trp	Gly	Leu	Val	Gly	Ala	Ile	
				485					490					495	
Ala	Tyr	Ala	Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
				500					505					510	
Val	Leu	Leu	Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
				515					520					525	
Leu	Trp	Lys	Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
				530					535					540	
Thr	Leu	Phe	Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
				545					550					555	
Arg	Leu	Ala	Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
				560					565					570	
Arg	Ala	Thr	Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
				575					580					585	
Val	Gln	Leu	His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
				590					595					600	
Thr	Met	Pro	Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
				605					610					615	
His	Asn	Gly	Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
				620					625					630	
Cys	Thr	Arg	Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
				635					640					645	
Pro	Val	Cys	His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
				650					655					660	
Val	Gly	Gly	Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
				665					670					675	
Ala	Leu	Val	Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
				680					685					690	
Tyr	Gly	Asn	Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
				695					700					705	
Trp	Gly	Leu	Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
				710					715					720	
Leu	Ala	Ser	Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
				725					730					735	

Val Ser Gly Ala	Ser Met Val Leu Pro Arg Ala Val Ala Gly Leu	740	745	750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu Trp Lys Pro Val Thr Val	755	760	765
Leu Val Lys Ala	Gly Ala Gly Ala Pro Arg Thr Arg Thr Val Leu	770	775	780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser Gln Ala Asp Leu Asp Tyr	785	790	795
Val Val Pro Gln	Ile Tyr Arg His Met Gln Glu Glu Phe Arg Gly	800	805	810
Arg Leu Glu Arg	Thr Lys Ser Gln Gly Pro Leu Thr Val Ala Ala	815	820	825
Tyr Gln Leu Gly	Ser Val Tyr Ser Ala Ala Met Val Thr Ala Leu	830	835	840
Thr Leu Leu Ala	Phe Pro Leu Leu Leu Leu His Ala Glu Arg Ile	845	850	855
Ser Leu Val Phe	Leu Leu Leu Phe Leu Gln Ser Phe Leu Leu Leu	860	865	870
His Leu Leu Ala	Ala Gly Ile Pro Val Thr Thr Pro Gly Pro Phe	875	880	885
Thr Val Pro Trp	Gln Ala Val Ser Ala Trp Ala Leu Met Ala Thr	890	895	900
Gln Thr Phe Tyr	Ser Thr Gly His Gln Pro Val Phe Pro Ala Ile	905	910	915
His Trp His Ala	Ala Phe Val Gly Phe Pro Glu Gly His Gly Ser	920	925	930
Cys Thr Trp Leu	Pro Ala Leu Leu Val Gly Ala Asn Thr Phe Ala	935	940	945
Ser His Leu Leu	Phe Ala Val Gly Cys Pro Leu Leu Leu Leu Trp	950	955	960
Pro Phe Leu Cys	Glu Ser Gln Gly Leu Arg Lys Arg Gln Gln Pro	965	970	975
Pro Gly Asn Glu	Ala Asp Ala Arg Val Arg Pro Glu Glu Glu Glu	980	985	990
Glu Pro Leu Met	Glu Met Arg Leu Arg Asp Ala Pro Gln His Phe	995	1000	1005
Tyr Ala Ala Leu	Leu Gln Leu Gly Leu Lys Tyr Leu Phe Ile Leu	1010	1015	1020

Gly Ile Gln Ile Leu Ala Cys Ala Leu Ala Ala Ser Ile Leu Arg		
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe Ala Pro Lys Phe Ile Phe		
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser Val Gly Leu Leu Leu Gly		
1055	1060	1065
Ile Ala Leu Val Met Arg Val Asp Gly Ala Val Ser Ser Trp Phe		
1070	1075	1080
Arg Gln Leu Phe Leu Ala Gln Gln Arg		
1085		

<210> 103
 <211> 1743
 <212> DNA
 <213> Homo sapiens

<400> 103
 tgcgcgtgcc gccgcgtgctg ctgttgctcc tggcggcgcc ttggggacgg 50
 gcagttccct gtgtctctgg tggtttgcc aaacctgcaa acatcacctt 100
 cttatccatc aacatgaaga atgtcctaca atggactcca ccagaggggc 150
 ttcaaggagt taaagttact tacactgtgc agtatttcat cacaaattgg 200
 cccaccagag gtggcaactga ctacagatga gaagtccatt totgttgctc 250
 tgacagctcc agagaagtgg aagagaaaac cagaagacct toctgtttcc 300
 atgcaacaaa tatactccaa totgaagtat aacgtgtctg tgttgaatac 350
 taaatcaaac agaagtggt cccagtgtgt gaccaaccac acgctggtgc 400
 tcaactggct ggagccgaac actctttact gcgtacagct ggagtccttc 450
 gtcccagggc cccctcgccg tgctcagcct tctgagaagc agtgtgccc 500
 gactttgaaa gatcaatcat cagagttcaa ggctaaaac atctttctgt 550
 atgttttgcc catatctatt accgtgtttc tttttctgt gatgggat 600
 tccatctacc gatatatcca cgttgcaaa gagaaacacc cagcaaattt 650
 gattttgatt tatggaaatg aatttgacaa aagattcttt gtgcctgctg 700
 aaaaaatcgt gattaacttt atcacctca atatctogga tgattctaaa 750
 atttctcatc aggatatgag tttactggga aaaagcagtg atgtatccag 800
 ccttaatgat cctcagcca gcgggaacct gagggccct caggaggaag 850
 aggaggtgaa acatttaggg tatgcttcgc atttgatgga aattttttgt 900

gactctgaag aaaacacgga aggtacttct ctcacccagc aagagtcctt 950
cagcagaaca atacccccgg ataaaacagt cattgaatat gaatatgatg 1000
tcagaaccac tgacatttgt gcggggcctg aagagcagga gctcagtttg 1050
caggaggagg tgtccacaca aggaacatta ttggagtcgc aggcagcggt 1100
ggcagtcttg ggcccgcaaa cgttacagta ctcatacacc cctcagctcc 1150
aagacttaga ccccttggcg caggagcaca cagactcgga ggaggggccc 1200
gaggaagagc catcgacgac cctggtcgac tgggatcccc aaactggcag 1250
gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300
agccttctga gggggatggg ctcgagagg agggcttctt atctagactc 1350
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catgcaattc atggaggaat ggggggtata tgtgcagatg gaaaactgat 1450
gccaacactt ccttttgctt ttgttttct gtgcaaaca gtgagtcacc 1500
cctttgatcc cagccataaa gtacctggga tgaaagaagt ttttccagt 1550
ttgtcagtggt ctgtgagaat tacttatttc ttttctctat tctcatagca 1600
cgtgtgtgat tggttcatgc atgtaggtct cttacaatg atgggtgggc 1650
tctggagtcc aggggctggc cggttgttct atgcagagaa agcagtcaat 1700
aaatgtttgc cagactgggt gcagaattta ttcaggtggg tgt 1743

<E10> 104

<E11> 442

<E12> PRT

<E13> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30

Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45

Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60

Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75

Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90

Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val	95	100	105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro	110	115	120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu	125	130	135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile	140	145	150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr	155	160	165
Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	170	175	180
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	185	190	195
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	200	205	210
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	215	220	225
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	230	235	240
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	245	250	255
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	260	265	270
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	275	280	285
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	290	295	300
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	305	310	315
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	320	325	330
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	335	340	345
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	350	355	360
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	365	370	375

Gly Arg Leu Cys Ile Pro Ser Leu Ser Ser Phe Asp Gln Asp Ser
380 385 390

Glu Gly Cys Glu Pro Ser Glu Gly Asp Gly Leu Gly Glu Glu Gly
395 400 405

Leu Leu Ser Arg Leu Tyr Glu Glu Pro Ala Pro Asp Arg Pro Pro
410 415 420

Gly Glu Asn Glu Thr Tyr Leu Met Gln Phe Met Glu Glu Trp Gly
425 430 435

Leu Tyr Val Gln Met Glu Asn
440

<210> 105

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 105

cgetgctgct gttgctcctg g 21

<210> 106

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 106

cagtgtgccca ggactttg 18

<210> 107

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 107

agtcgcaggc agcgttgg 18

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 108
ctctccgag tctgtgtgct cctgc 25

<210> 109

<211> 51

<212> DNA

<213> Artificial Sequence

<200>

<213> Synthetic oligonucleotide probe

<400> 109

ggacgggcag ttccctgtgt ctctgggtgt ttgcctaaac ctgcaaacad 50

c 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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tctgctgact gtggccaccg cctgatgct gcccgtaag cccccgcag 150
gtctctgggg ggcccagatc atcgggggccc acgaggtgac cccccactcc 200
aggccctaca tggcatcctg gcgcttcggg ggccaacatc actgcggagg 250
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acagagacct ccgcactggc ctgggtgggtgc tgggcgccc cgtcctgagt 350
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ccccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
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tggtcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
tgcaaagggc agaagcaaac ccagtaaaat gttaactgac aaaaaaaaaa 1100
aaaaaaaaaa gaaa 1114

<210> 111
<211> 283
<212> PRT
<213> Homo sapiens

<400> 111
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20 25 30
Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45
Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60
Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75
Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90
His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105
Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120
Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135
Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150
Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165
Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180
Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195
Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg

200	205	210
Arg Gly Phe Cys Ser Ala Asp Ser Gly	Gly Pro Leu Val Cys Arg	
215	220	225
Asn Arg Ala His Gly Leu Val Ser Phe	Ser Gly Leu Trp Cys Gly	
230	235	240
Asp Pro Lys Thr Pro Asp Val Tyr Thr	Gln Val Ser Ala Phe Val	
245	250	255
Ala Trp Ile Trp Asp Val Val Arg Arg	Ser Ser Pro Gln Pro Gly	
260	265	270
Pro Leu Pro Gly Thr Thr Arg Pro Pro	Gly Glu Ala Ala	
275	280	

<210> 112
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 112
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<210> 113
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 113
 cgagaaggaa acgaggccgt gag 23

<210> 114
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 114
 tgacacttac catgctctgc acccgagtg gggacagcca caga 44

<210> 115
 <211> 1808
 <212> DNA
 <213> Homo sapiens

<400> 115
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cgctgtcggc gctgggcacg gtagcaggcg ccgcctgtct gctcaaggac 150
tatgtcaccg gtggggcttg cccagcaag gccaccatcc ctgggaagac 200
ggtcacgtg acgggcgcca acacaggcat cgggaagcag accgccttgg 250
aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300
aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350
tgtcaacgcc cggcacctgg acttggttcc cctcaagtct atccgagagt 400
ttgcagcaaa gatcattgaa gaggaggagc gagtggacat tctaataaac 450
aacgcgggtg tgatgcggtg cccccactgg accaccgagg acggcttcga 500
gatgcagttt ggcgttaacc acctgggtca ctttctcttg acaaacttgc 550
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tctgacactt ggtggattct tgggtccctg tgggaccttg tgcattgcatg 1500
gtcctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550
ctgtctccca tgatggtgtg gtacagcgag ctgttgctctg gctatggcat 1600
ggctgtgccg ggggtgtttg ctgagggctt cctgtgccag agcccagcca 1650
gagagcaggt gcaggtgtca tcccagattc aggcctctgca cggcatggag 1700
tgggaacccc accagctgct gctacaggac ctgggattgc ctgggactcc 1750
caccttccta tcaattctca tggtagtcca aactgcagac tctcaaactt 1800
gctcattt 1808

<210> 116
<211> 331
<212> PRT
<213> Homo sapiens

<400> 116
Met Ser Arg Tyr Leu Leu Pro Leu Ser Ala Leu Gly Thr Val Ala
1 5 10 15
Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
20 25 30
Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
35 40 45
Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
50 55 60
Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
65 70 75
Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
80 85 90
Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
95 100 105
Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
110 115 120
Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
125 130 135
Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
140 145 150
Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
155 160 165
Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
170 175 180

His	Ile	Asp	Phe	Asp	Asp	Leu	Asn	Trp	Gln	Thr	Arg	Lys	Tyr	Asn
				185					190					195
Thr	Lys	Ala	Ala	Tyr	Cys	Gln	Ser	Lys	Leu	Ala	Ile	Val	Leu	Phe
				200					205					210
Thr	Lys	Glu	Leu	Ser	Arg	Arg	Leu	Gln	Gly	Ser	Gly	Val	Thr	Val
				215					220					225
Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117
 <211> 2249
 <212> DNA
 <213> Homo sapiens

<400> 117
 gaagttcgcg agcgcctggca tgtggtcctg gggcgcggtt ggcggcgctg 50
 ctggcggtgc tggcgctcgg gacaggagac ccagaaaggg ctgcggctcg 100
 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgcccg 150
 agcgccgggt gctggggctg ctgaggcggt acctgcgcgg ggaggaggcg 200
 cggctgcggg acctgactag attctacgac aaggtacttt ctttgcata 250
 ggattcaaca acccctgtgg ctaaccctct gcttgcattt actctcatca 300
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
 gagaacatcc gagctctgaa ggatggctat gagaagggtg agcaagacct 400
 tccagccttt gaggaccttg agggagcagc aagggcctg atgcggctgc 450

aggacgtgta catgctcaat gtgaaaggcc tggcccgagg tgtctttcag 500
 agagtcactg gctctgccat cactgacctg tacagcccca aacggctctt 550
 ttctctcaca ggggatgact gcttccaagt tggcaagggtg gcctatgaca 600
 tgggggatta ttaccatgcc attccatggc tggaggaggc tgtcagtctc 650
 ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700
 agatgccttg gatcacttg cctttgctta tttccgggca ggaaatgttt 750
 cgtgtgccct cagcctctct cgggagtttc ttctctacag cccagataat 800
 aagaggatgg ccaggaatgt cttgaaatat gaaaggctct tggcagagag 850
 ccccaaccac gtggtagctg aggctgtcat ccagaggccc aatatacccc 900
 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950
 cageccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000
 ttccaacgcc tacctgctgc tccagcccat ccggaaggag gtcattccacc 1050
 tggagcccta cattgctctc taccatgact tcgtcagtga ctcagaggct 1100
 cagaaaatta gagaacttgc agaaccatgg ctacagaggt cagtgggtggc 1150
 atcaggggag aagcagttac aagtggagta ccgcatcagc aaaagtgcct 1200
 ggctgaagga cactgttgac ccaaaactgg tgacctcaa ccaccgcatt 1250
 gctgccctca caggccttga tgtccggcct ccctatgcag agtatctgca 1300
 ggtggtgaac tatggcatcg gaggacacta tgagcctcac tttgaccatg 1350
 ctacgtcacc aagcagcccc ctctacagaa tgaagtcagg aaaccgagtt 1400
 gcaacattta tgatctatct gagctcgggtg gaagctggag gagccacagc 1450
 cttcatctat gccaacctca gcgtgcctgt ggtaggaat gcagcactgt 1500
 tttggtggaa cctgcacagg agtgggtgaag gggacagtga cacacttcat 1550
 gctggctgtc ctgtcctggt gggagataag tgggtggcca acaagtggat 1600
 acatgagtat ggacaggaat tccgcagacc ctgcagctcc agccctgaag 1650
 actgaactgt tggcagagag aagctggtgg agtcctgtgg ctttccagag 1700
 aagccaggag ccaaaagctg gggtaggaga ggagaaagca gagcagcctc 1750
 ctggaagaag gccttgtcag ctttgtctgt gcctcgcaaa tcagaggcaa 1800
 gggagaggtt gttaccaggg gacactgaga atgtacattt gatctgcccc 1850

agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtgga 1900
ggcctgagag ggaagtttct ggagttcaga tactctctgt tggaacagg 1950
acatctcaac agtctcaggt tcgatcagtg ggtcttttgg cactttgaac 2000
cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050
tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100
agcccaagca gggagtgtcc cctccccaaga agcatatccc agatgagtgg 2150
tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200
tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala	1	5	10	15
Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr	20	25	30	
Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg	35	40	45	
Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala	50	55	60	
Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu	65	70	75	
His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe	80	85	90	
Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His	95	100	105	
Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr	110	115	120	
Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly	125	130	135	
Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn	140	145	150	
Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser	155	160	165	
Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr	170	175	180	

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly	185	190	195
Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu	200	205	210
Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser	215	220	225
Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala	230	235	240
Gly Asn Val Ser Cys Ala Leu Ser Leu Ser Arg Glu Phe Leu Leu	245	250	255
Tyr Ser Pro Asp Asn Lys Arg Met Ala Arg Asn Val Leu Lys Tyr	260	265	270
Glu Arg Leu Leu Ala Glu Ser Pro Asn His Val Val Ala Glu Ala	275	280	285
Val Ile Gln Arg Pro Asn Ile Pro His Leu Gln Thr Arg Asp Thr	290	295	300
Tyr Glu Gly Leu Cys Gln Thr Leu Gly Ser Gln Pro Thr Leu Tyr	305	310	315
Gln Ile Pro Ser Leu Tyr Cys Ser Tyr Glu Thr Asn Ser Asn Ala	320	325	330
Tyr Leu Leu Leu Gln Pro Ile Arg Lys Glu Val Ile His Leu Glu	335	340	345
Pro Tyr Ile Ala Leu Tyr His Asp Phe Val Ser Asp Ser Glu Ala	350	355	360
Gln Lys Ile Arg Glu Leu Ala Glu Pro Trp Leu Gln Arg Ser Val	365	370	375
Val Ala Ser Gly Glu Lys Gln Leu Gln Val Glu Tyr Arg Ile Ser	380	385	390
Lys Ser Ala Trp Leu Lys Asp Thr Val Asp Pro Lys Leu Val Thr	395	400	405
Leu Asn His Arg Ile Ala Ala Leu Thr Gly Leu Asp Val Arg Pro	410	415	420
Pro Tyr Ala Glu Tyr Leu Gln Val Val Asn Tyr Gly Ile Gly Gly	425	430	435
His Tyr Glu Pro His Phe Asp His Ala Thr Ser Pro Ser Ser Pro	440	445	450
Leu Tyr Arg Met Lys Ser Gly Asn Arg Val Ala Thr Phe Met Ile	455	460	465

Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr
				470					475					480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp
				485					490					495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His
				500					505					510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys
				515					520					525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser
				530					535					540

Ser Pro Glu Asp

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 119
 ggggacagga gaccagaaa ggg 23

<210> 120
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 121
 ctgggggacc tgactagatt ctacgacaag gtactttctt tgcattgggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122

gagatagggg gtctgggttt aagttcctgc tccatctcag gagccctgc 50
tcccacccct aggaagccac cagactccac ggtgtggggc caatcaggtg 100
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
ggagagcccc ggagcccccg taaccgcgcg ggggagcgcc caggatgccg 200
cgcggggact cggagcaggt gcgctaactg gcgcgcttct cctacctctg 250
gctcaagttt tcaattatca tctattccac cgtgttctgg ctgattgggg 300
ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350
aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatcctct 400
ggcgctcgtc atgttcattg tctccttcat tgggtgtctg gcgtccctcc 450
gtgacaaact gtaccttctc caagcattca tgtacatcct tgggatctgc 500
ctcatcatgg agctcattgg tggcgtgggt gccttgacct tccggaacca 550
gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600
atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650
aagtgtctgt ggggggagga ctaccgagat tggagcaaga atcagtacca 700
cgactgcagt gccctggac cctggcctg tgggtgccc tacacctgt 750
gcatcaggaa caggacagaa gttgtcaaca ccatgtctgg ctacaaaact 800
atcgacaagg agcgtttcag tgtgcaggat gtcactctac tgcggggctg 850
caccaacgcc gtgatcatct ggttcattga caactacacc atcatggcgt 900
gcatcctctt gggcatcctg ctccccagt tctgggggt gctgctgacg 950
ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050
cgggatgctg cttgtgtac cccaattagg gccagcctg ccatggcagc 1100
tccaacaagg accgtctggg atagcacctc tcagtcaaca tctggggct 1150
ggacagggt gcggccctc tgcccacact cagtactgac caaagccagg 1200
gctgtgtgtg cctgtgtgta ggtcccaagg cctctgcctc ccaggggagc 1250
agagcctggg cctcccctaa gaggtttcc ccgaggcagc tctggaatct 1300
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ctacagggga ggagagcct gaggtctctg tcagggccca ttcatctct 1400

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 gggcaggagg gaagagctgt ccatgcagcc acgcccattgg ccagggttggc 1550
 ctctttctcag cctcccaggt gccttgagcc ctcttgcaag ggcgggtgct 1600
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650
 gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700
 gtcttattct tgcctttccc ccaaccagtt tgттаатcaa асаатааааа 1750
 catgttttgt tttgttttta аааааааа 1778

<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe	1	5	10	15
Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val	20	25	30	
Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala	35	40	45	
Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu	50	55	60	
Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met	65	70	75	
Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr	80	85	90	
Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met	95	100	105	
Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr	110	115	120	
Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr	125	130	135	
Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys	140	145	150	
Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys	155	160	165	
Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly				

170	175	180
Val Pro Tyr Thr Cys Cys Ile Arg Asn	Thr Thr Glu Val Val Asn	
185	190	195
Thr Met Cys Gly Tyr Lys Thr Ile Asp	Lys Glu Arg Phe Ser Val	
200	205	210
Gln Asp Val Ile Tyr Val Arg Gly Cys	Thr Asn Ala Val Ile Ile	
215	220	225
Trp Phe Met Asp Asn Tyr Thr Ile Met	Ala Cys Ile Leu Leu Gly	
230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 124

atcatctatt ccacgtgtt ctggc 25

<210> 125

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gacagagtgc tccatgatga tgtcc 25

<210> 126

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127

<211> 1636

<212> DNA

<213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcttgcactt 50

gctgcccctct gacacctggg aagatggccg gcccgaggac cttcacccctt 100

ctctgtgggtt tgetggcagc caccttgatc caagccaccc tcagtccac 150

tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200

agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250

agtjccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300

gggtgaacacc gtctgaagc acatcatctg gctgaaggct atcacagcta 350

acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400

gtcaagatcc ccttggacat ggtggctgga ttcaaacgc ccctgggtcaa 450

gaccatcgtg gagttccaca tgacgactga ggcccaagcc accatccgca 500

tggacaccag tgcaagtggc ccacccgcc tggctctcag tgactgtgcc 550

accagccatg ggagcctgcg catccaactg ctgtataagc tctccttct 600

gggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650

ccaatctagt gaaaaaccag ctgtgtcccg tgatcaggc ttccttcaat 700

ggcatgtatg cagacctct gcagctgggtg aagggtgcca tttccctcag 750

cattgaaccgt ctggagtttg accttctgta tcttgccatc aagggtgaca 800

ccattcagct ctacctggg gccagttgt tggactcaca gggaaagggtg 850

accaagtgggt tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900

caacatcccg ttcagcctca tcgtgagtca ggacgtgggtg aaagctgcag 950

tggctgtgtg gctctctcca gaagaattca tggctctgtt ggactctgtg 1000

cttctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050

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aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150

ctgatcgtgc tggaagtgtt tccctccagt gaagccctcc gccctttgtt 1200

caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250

accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300
 atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350
 cactgagatc atccactcca tcttgctgcc gaaccagaat ggcaaattaa 1400
 gatctggggg cccagtgtca ttggtgaagg ccttgggatt cgaggcagct 1450
 gagtcctcac tgaccaagga tgcccttgctg cttactccag cctccttgctg 1500
 gaaaccagc tctcctgtct cccagtgaag acttggtatgg cagccatcag 1550
 ggaaggctgg gtcccagctg ggagtatggg tgtgagctct atagaccatc 1600
 cctctctgca atcaataaac acttgctgtg gaaaaa 1636

<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala
 1 5 10 15
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile
 20 25 30
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys
 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu

	170	175	180
Ala Lys Gln Val	Met Asn Leu Leu Val	Pro Ser Leu Pro Asn Leu	
	185	190	195
Val Lys Asn Gln	Leu Cys Pro Val Ile	Glu Ala Ser Phe Asn Gly	
	200	205	210
Met Tyr Ala Asp	Leu Leu Gln Leu Val	Lys Val Pro Ile Ser Leu	
	215	220	225
Ser Ile Asp Arg	Leu Glu Phe Asp Leu	Leu Tyr Pro Ala Ile Lys	
	230	235	240
Gly Asp Thr Ile	Gln Leu Tyr Leu Gly	Ala Lys Leu Leu Asp Ser	
	245	250	255
Gln Gly Lys Val	Thr Lys Trp Phe Asn	Asn Ser Ala Ala Ser Leu	
	260	265	270
Thr Met Pro Thr	Leu Asp Asn Ile Pro	Phe Ser Leu Ile Val Ser	
	275	280	285
Gln Asp Val Val	Lys Ala Ala Val Ala	Ala Val Leu Ser Pro Glu	
	290	295	300
Glu Phe Met Val	Leu Leu Asp Ser Val	Leu Pro Glu Ser Ala His	
	305	310	315
Arg Leu Lys Ser	Ser Ile Gly Leu Ile	Asn Glu Lys Ala Ala Asp	
	320	325	330
Lys Leu Gly Ser	Thr Gln Ile Val Lys	Ile Leu Thr Gln Asp Thr	
	335	340	345
Pro Glu Phe Phe	Ile Asp Gln Gly His	Ala Lys Val Ala Gln Leu	
	350	355	360
Ile Val Leu Glu	Val Phe Pro Ser Ser	Glu Ala Leu Arg Pro Leu	
	365	370	375
Phe Thr Leu Gly	Ile Glu Ala Ser Ser	Glu Ala Gln Phe Tyr Thr	
	380	385	390
Lys Gly Asp Gln	Leu Ile Leu Asn Leu	Asn Asn Ile Ser Ser Asp	
	395	400	405
Arg Ile Gln Leu	Met Asn Ser Gly Ile	Gly Trp Phe Gln Pro Asp	
	410	415	420
Val Leu Lys Asn	Ile Ile Thr Glu Ile	Ile His Ser Ile Leu Leu	
	425	430	435
Pro Asn Gln Asn	Gly Lys Leu Arg Ser	Gly Val Pro Val Ser Leu	
	440	445	450
Val Lys Ala Leu	Gly Phe Glu Ala Ala	Glu Ser Ser Leu Thr Lys	

455

460

465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser
 470 475 480

Pro Val Ser Gln

(C10) 129

(C11) 2213

(C12) DNA

(C13) Homo sapiens

(C400) 129

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<210> 130

<211> 335

<212> PRT

<213> Homo sapiens

<400> 130

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20	25	30
Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met		
35	40	45
Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys		
50	55	60
Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile		
65	70	75
Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys		
80	85	90
Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg		
95	100	105
Tyr Ser Ser Ala Phe Thr Asn Arg Ile Phe Phe Ala Met Val Asp		
110	115	120
Phe Asp Glu Gly Ser Asp Val Phe Gln Met Leu Asn Met Asn Ser		
125	130	135
Ala Pro Thr Phe Ile Asn Phe Pro Ala Lys Gly Lys Pro Lys Arg		
140	145	150
Gly Asp Thr Tyr Glu Leu Gln Val Arg Gly Phe Ser Ala Glu Gln		
155	160	165
Ile Ala Arg Trp Ile Ala Asp Arg Thr Asp Val Asn Ile Arg Val		
170	175	180
Ile Arg Pro Pro Asn Tyr Ala Gly Pro Leu Met Leu Gly Leu Leu		
185	190	195
Leu Ala Val Ile Gly Gly Leu Val Tyr Leu Arg Arg Ser Asn Met		
200	205	210
Glu Phe Leu Phe Asn Lys Thr Gly Trp Ala Phe Ala Ala Leu Cys		
215	220	225
Phe Val Leu Ala Met Thr Ser Gly Gln Met Trp Asn His Ile Arg		
230	235	240
Gly Pro Pro Tyr Ala His Lys Asn Pro His Thr Gly His Val Asn		
245	250	255
Tyr Ile His Gly Ser Ser Gln Ala Gln Phe Val Ala Glu Thr His		
260	265	270
Ile Val Leu Leu Phe Asn Gly Gly Val Thr Leu Gly Met Val Leu		
275	280	285
Leu Cys Glu Ala Ala Thr Ser Asp Met Asp Ile Gly Lys Arg Lys		
290	295	300
Ile Met Cys Val Ala Gly Ile Gly Leu Val Val Leu Phe Phe Ser		

305	310	315
Trp Met Leu Ser Ile Phe Arg Ser Lys Tyr His Gly Tyr Pro Tyr		
320	325	330
Ser Phe Leu Met Ser		
335		

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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 cttggcgctg gcggtactgg cccccggagc aggggagcag aggcggagag 200
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
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 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400
 ttaacagaat cttggaataa ttttaagggt ctagatccaa attatacaac 450
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 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
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 taatcttatt cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
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 ctcagaggct gaggcaggag gatcgcttga acccgggagg cagcagttgc 2050
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 aaaaaaaaaa aaaaaaaaaa aaaaaa 2476

<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132

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Val	Leu	Ala	Pro	Gly	Ala	Gly	Glu	Gln	Arg	Arg	Arg	Ala	Ala	Lys	
				20					25					30	
Ala	Pro	Asn	Val	Val	Leu	Val	Val	Ser	Asp	Ser	Phe	Asp	Gly	Arg	
				35					40					45	
Leu	Thr	Phe	His	Pro	Gly	Ser	Gln	Val	Val	Lys	Leu	Pro	Phe	Ile	
				50					55					60	
Asn	Phe	Met	Lys	Thr	Arg	Gly	Thr	Ser	Phe	Leu	Asn	Ala	Tyr	Thr	
				65					70					75	
Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	

Tyr Ser Ser Tyr Thr Lys Asn Cys Thr Gly Arg Phe Thr Lys Lys	260	265	270
Glu Ile Lys Asn Ile Arg Ala Phe Tyr Tyr Ala Met Cys Ala Glu	275	280	285
Thr Asp Ala Met Leu Gly Glu Ile Ile Leu Ala Leu His Gln Leu	290	295	300
Asp Leu Leu Gln Lys Thr Ile Val Ile Tyr Ser Ser Asp His Gly	305	310	315
Glu Leu Ala Met Glu His Arg Gln Phe Tyr Lys Met Ser Met Tyr	320	325	330
Glu Ala Ser Ala His Val Pro Leu Leu Met Met Gly Pro Gly Ile	335	340	345
Lys Ala Gly Leu Gln Val Ser Asn Val Val Ser Leu Val Asp Ile	350	355	360
Tyr Pro Thr Met Leu Asp Ile Ala Gly Ile Pro Leu Pro Gln Asn	365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys	380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser	395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg	410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile	425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr	440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln	455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val	470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile	485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln	500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln	515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val	530	535	

<210> 133
<211> 1475
<212> DNA
<213> Homo sapiens

<400> 133
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catcaccag tgtgacatct atagaccct tctgggctg ccgctgaca 350
tccaggtgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
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 gcagcctggg acatttaaaa aaata 1475

<210> 134
 <211> 230
 <212> PRT
 <213> Homo sapiens

<400> 134
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 Leu Gly Leu Leu Gly Thr Leu Val Ala Met Leu Leu Pro Ser Trp 30
 20 25
 Lys Thr Ser Ser Tyr Val Gly Ala Ser Ile Val Thr Ala Val Gly 45
 35 40
 Phe Ser Lys Gly Leu Trp Met Glu Cys Ala Thr His Ser Thr Gly 60
 50 55
 Ile Thr Gln Cys Asp Ile Tyr Ser Thr Leu Leu Gly Leu Pro Ala 75
 65 70
 Asp Ile Gln Ala Ala Gln Ala Met Met Val Thr Ser Ser Ala Ile 90
 80 85
 Ser Ser Leu Ala Cys Ile Ile Ser Val Val Gly Met Arg Cys Thr 105
 95 100
 Val Phe Cys Gln Glu Ser Arg Ala Lys Asp Arg Val Ala Val Ala 120
 110 115
 Gly Gly Val Phe Phe Ile Leu Gly Gly Leu Leu Gly Phe Ile Pro 135
 125 130
 Val Ala Trp Asn Leu His Gly Ile Leu Arg Asp Phe Tyr Ser Pro 150
 140 145
 Leu Val Pro Asp Ser Met Lys Phe Glu Ile Gly Glu Ala Leu Tyr 165
 155 160
 Leu Gly Ile Ile Ser Ser Leu Phe Ser Leu Ile Ala Gly Ile Ile 180
 170 175
 Leu Cys Phe Ser Cys Ser Ser Gln Arg Asn Arg Ser Asn Tyr Tyr 195
 185 190
 Asp Ala Tyr Gln Ala Gln Pro Leu Ala Thr Arg Ser Ser Pro Arg 210
 200 205

Pro Gly Gln Pro Pro Lys Val Lys Ser Glu Phe Asn Ser Tyr Ser
 215 220 225

Leu Thr Gly Tyr Val
 230

<210> 135
 <211> 610
 <212> DNA
 <213> Homo sapiens

<400> 135
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 aggtgtggag acaagatcta caacccttg gagcagtgt gttacaatga 200
 cggcatcgtg tccctgagcg agaccgcga atgtgggtccc cctgcacct 250
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 aggtaatatg tgtaccagta gagaagcctg aggaatttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
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 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
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 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys

	65		70		75									
Phe	Glu	Leu	Cys	Cys	Leu	Asp	Ser	Phe	Gly	Leu	Thr	Asn	Asp	Phe
			80						85					90
Val	Val	Lys	Leu	Lys	Val	Gln	Gly	Val	Asn	Ser	Gln	Cys	His	Ser
				95					100					105
Ser	Pro	Ile	Ser	Ser	Lys	Cys	Glu	Ser	Arg	Arg	Arg	Phe	Pro	
				110					115					

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500
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<210> 138
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 138
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 1 5 10 15

Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	
				20					25					30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	
				35					40					45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	
				50					55					60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	
				65					70					75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	
				80					85					90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	
				95					100					105	
Cys	Arg	Ser	Val	Ser											
				110											

<210> 139
 <211> 2044
 <212> DNA
 <213> Homo sapiens

<400> 139
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 cccacggccc tggaggccgg cagctggcgc tggggatccc tgctcttcgc 200
 tctcttctcg gctgcgtccc taggtccggt ggcagccttc aaggtcgcca 250
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<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly	1	5	10	15
Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val	20	25	30	
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro	35	40	45	
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val	50	55	60	
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser	65	70	75	
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg	80	85	90	
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln	95	100	105	
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu	110	115	120	
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn	125	130	135	
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu	140	145	150	
Ile	Arg	His	His	His	Ser	Glu	His	Arg	Val	His	Gly	Ala	Met	Glu	155	160	165	
Leu	Gln	Val	Gln	Thr	Gly	Lys	Asp	Ala	Pro	Ser	Asn	Cys	Val	Val	170	175	180	
Tyr	Pro	Ser	Ser	Ser	Gln	Asp	Ser	Glu	Asn	Ile	Thr	Ala	Ala	Ala	185	190	195	
Leu	Ala	Thr	Gly	Ala	Cys	Ile	Val	Gly	Ile	Leu	Cys	Leu	Pro	Leu	200	205	210	
Ile	Leu	Leu	Leu	Val	Tyr	Lys	Gln	Arg	Gln	Ala	Ala	Ser	Asn	Arg	215	220	225	
Arg	Ala	Gln	Glu	Leu	Val	Arg	Met	Asp	Ser	Asn	Ile	Gln	Gly	Ile	230	235	240	
Glu	Asn	Pro	Gly	Phe	Glu	Ala	Ser	Pro	Pro	Ala	Gln	Gly	Ile	Pro	245	250	255	
Glu	Ala	Lys	Val	Arg	His	Pro	Leu	Ser	Tyr	Val	Ala	Gln	Arg	Gln	260	265	270	
Pro	Ser	Glu	Ser	Gly	Arg	His	Leu	Leu	Ser	Glu	Pro	Ser	Thr	Pro				

	275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp			
	290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile			
	305	310	

<210> 141
 <211> 1732
 <212> DNA
 <213> Homo sapiens

<400> 141
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 cttagacctc ccttctgcc ctctttctt gccaccgct gcttctggc 150
 ccttctccga ccccgctcta gcagcagacc tctgggggc tgtgggtga 200
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 gatgtactgc ctgcctgta cctgctcaga gggcgcccat gtgagttgtt 500
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 cagcaatgct gtcccaagt tgtggaacct cacactcct ctggactccg 600
 ggccccacca aagtctgcc agcacaacgg gaccatgtac caacacggag 650
 agatcttcag tgcccatgag ctgttccct cccgctgcc caaccagtgt 700
 gtctctgca gctgcacaga gggccagatc tactgcggc tcacaacctg 750
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 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850
 cagtcgctcc atgggtgag acatcctcag gatccatgtt ccagtgatgc 900
 tgggagaaaag agaggcccg gcacccagc cccactggc ctacgcgcc 950
 ctctgagctt catcctgc cacttcagac ccaagggagc aggcagcaca 1000
 actgtcaaga tcgtctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050
 cgggaagacg tactccacg gggaggtgtg gcacccggc ttccgtgcct 1100

tgggcccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150
 tgccagcgtg tgacctgtcc caccgagtag cctgcccgtc accccgagaa 1200
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 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300
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 gaaggtoact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<110> 142

<111> 451

<112> PRT

<113> Homo sapiens

<110> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp
				20					25					30
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser
				35					40					45
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg
				50					55					60
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His
				65					70					75
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln
				80					85					90
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg
				95					100					105
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His
				110					115					120

Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	
				290					295					300	
Arg	His	Pro	Glu	Lys	Val	Ala	Gly	Lys	Cys	Cys	Lys	Ile	Cys	Pro	
				305					310					315	
Glu	Asp	Lys	Ala	Asp	Pro	Gly	His	Ser	Glu	Ile	Ser	Ser	Thr	Arg	
				320					325					330	
Cys	Pro	Lys	Ala	Pro	Gly	Arg	Val	Leu	Val	His	Thr	Ser	Val	Ser	
				335					340					345	
Pro	Ser	Pro	Asp	Asn	Leu	Arg	Arg	Phe	Ala	Leu	Glu	His	Glu	Ala	
				350					355					360	
Ser	Asp	Leu	Val	Glu	Ile	Tyr	Leu	Trp	Lys	Leu	Val	Lys	Asp	Glu	
				365					370					375	
Glu	Thr	Glu	Ala	Gln	Arg	Gly	Glu	Val	Pro	Gly	Pro	Arg	Pro	His	
				380					385					390	
Ser	Gln	Asn	Leu	Pro	Leu	Asp	Ser	Asp	Gln	Glu	Ser	Gln	Glu	Ala	
				395					400					405	

Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro
 410 415 420

Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala
 425 430 435

Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys
 440 445 450

Thr

<210> 143

<211> 693

<212> DNA

<213> Homo sapiens

<400> 143

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 cttgcggaaa atgctgatct cagtcgcaat gctggjcgca ggggctggcg 150
 tgggctacgc gctcctcggt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
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 gaccttggtt tgggjcagcg aatccgaggc agcctttctc cttcgtgggc 450
 ccagcggaga gtcgggaccg agataccatg ccaggactct ccggggtcct 500
 gtgagctgcc gtcgggtgag cacttttccc ccaaaccctg gactgactgc 550
 ttttaaggtec gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 aactgaaaga accaataaaa tcatgttcc ccaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144

<211> 93

<212> PRT

<213> Homo sapiens

<400> 144

Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
 1 5 10 15

Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30

Gly	Glu	Arg	Arg	Lys	Gln	Glu	Met	Leu	Lys	Glu	Met	Pro	Leu	Gln	
				35					40					45	
Asp	Pro	Arg	Ser	Arg	Glu	Glu	Ala	Ala	Arg	Thr	Gln	Gln	Leu	Leu	
				50					55					60	
Leu	Ala	Thr	Leu	Gln	Glu	Ala	Ala	Thr	Thr	Gln	Glu	Asn	Val	Ala	
				65					70					75	
Trp	Arg	Lys	Asn	Trp	Met	Val	Gly	Gly	Glu	Gly	Gly	Ala	Ser	Gly	
				80					85					90	

Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggctgact gtacgttcct tctactctgg caccactctc 100
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 atggctggga cccctccaag gacagcagca ccaccttggt gagtacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
 agtagtcggc atgtgtctga gctgcgggac ttcaagaaca agatgctgcc 300
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350
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 aaccgaacag tggtaggacag ctgagtattc ccagcagagg ggetgatccc 900

cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950
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 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350
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 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
1				5					10					15

Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20				25						30

Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35				40						45

Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Lys Met Leu Pro Leu Leu Glu Val Ala	Glu Lys Glu Arg Glu Ala	
65	70	75
Leu Arg Thr Glu Ala Asp Thr Ile Ser	Gly Arg Val Asp Arg Leu	
80	85	90
Glu Arg Glu Val Asp Tyr Leu Glu Thr	Gln Asn Pro Ala Leu Pro	
95	100	105
Cys Val Glu Phe Asp Glu Lys Val Thr	Gly Gly Pro Gly Thr Lys	
110	115	120
Gly Lys Gly Arg Arg Asn Glu Lys Tyr	Asp Met Val Thr Asp Cys	
125	130	135
Gly Tyr Thr Ile Ser Gln Val Arg Ser	Met Lys Ile Leu Lys Arg	
140	145	150
Phe Gly Gly Pro Ala Gly Leu Trp Thr	Lys Asp Pro Leu Gly Gln	
155	160	165
Thr Glu Lys Ile Tyr Val Leu Asp Gly	Thr Gln Asn Asp Thr Ala	
170	175	180
Phe Val Phe Pro Arg Leu Arg Asp Phe	Thr Leu Ala Met Ala Ala	
185	190	195
Arg Lys Ala Ser Arg Val Arg Val Pro	Phe Pro Trp Val Gly Thr	
200	205	210
Gly Gln Leu Val Tyr Gly Gly Phe Leu	Tyr Phe Ala Arg Arg Pro	
215	220	225
Pro Gly Arg Pro Gly Gly Gly Gly Glu	Met Glu Asn Thr Leu Gln	
230	235	240
Leu Ile Lys Phe His Leu Ala Asn Arg	Thr Val Val Asp Ser Ser	
245	250	255
Val Phe Pro Ala Glu Gly Leu Ile Pro	Pro Tyr Gly Leu Thr Ala	
260	265	270
Asp Thr Tyr Ile Asp Leu Val Ala Asp	Glu Glu Gly Leu Trp Ala	
275	280	285
Val Tyr Ala Thr Arg Glu Asp Asp Arg	His Leu Cys Leu Ala Lys	
290	295	300
Leu Asp Pro Gln Thr Leu Asp Thr Glu	Gln Gln Trp Asp Thr Pro	
305	310	315
Cys Pro Arg Glu Asn Ala Glu Ala Ala	Phe Val Ile Cys Gly Thr	
320	325	330
Leu Tyr Val Val Tyr Asn Thr Arg Pro	Ala Ser Arg Ala Arg Ile	

335	340	345
Gln Cys Ser Phe Asp Ala Ser Gly Thr	Leu Thr Pro Glu Arg Ala	
350	355	360
Ala Leu Pro Tyr Phe Pro Arg Arg Tyr	Gly Ala His Ala Ser Leu	
365	370	375
Arg Tyr Asn Pro Arg Glu Arg Gln Leu	Tyr Ala Trp Asp Asp Gly	
380	385	390
Tyr Gln Ile Val Tyr Lys Leu Glu Met	Arg Lys Lys Glu Glu Glu	
395	400	405

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 gttctcctct tctctetaat ccatccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300
 gtttctgtgc tctaagacc aatgcagagg ccatggaagt gcggttcttc 350
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatztatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500
 ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550
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 tccatgcggc atgctcatct gagccgagag gtggaatcca ggttacagat 850

aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900
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 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150
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 cyatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
 cattaaatcc ccgttttata agcgtcttcc ccaggacccc acctacaaaa 1400
 ataggggtct tcctggacta tgagtgtggg accatctctt tcttcaacat 1450
 aaatgaccag tcccttattt ataccctgac atgtcggttt gaaggcttat 1500
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tctcacagg 1650
 caaccacgcc cttctcccc aggggtgaaa tgtaggatga atcacatccc 1700
 acattcttct ttagggatat taaggctctt ctcccagatc caaagtccc 1750
 cagcagccgg ccaagggtgc ttccagatga agggggactg gcctgtccac 1800
 atgggagtca ggtgtcatgg ctgccctgag ctgggagggg agaaggctga 1850
 cattacattt agtttgcctt cactccatct ggctaagtga tcttgaaata 1900
 ccacctctca ggtgaagaac cgtcaggaat tccatctca caggctgtgg 1950
 tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000
 acagagtgtg tctaattggt ttgttcatta tattacactt tcagtaaaaa 2050
 aa 2052

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly

1	5	10	15
Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala	20	25	30
Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys	35	40	45
Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe	50	55	60
Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe	65	70	75
Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp	80	85	90
Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr	95	100	105
Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser	110	115	120
Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly	125	130	135
Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile	140	145	150
Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala	155	160	165
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg	170	175	180
Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu	185	190	195
Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His	200	205	210
Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp	215	220	225
Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu	230	235	240
Gly Ile Leu Cys Cys Gly Leu Phe Phe Gly Ile Val Gly Leu Lys	245	250	255
Ile Phe Phe Ser Lys Phe Gln Trp Lys Ile Gln Ala Glu Leu Asp	260	265	270
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys	275	280	285
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys			

290	295	300
Leu Cys Val Ser Asp	Leu Lys Thr Val Thr His Arg Lys Ala	Pro
305	310	315
Gln Glu Val Pro His Ser Glu Lys Arg	Phe Thr Arg Lys Ser	Val
320	325	330
Val Ala Ser Gln Ser Phe Gln Ala Gly	Lys His Tyr Trp Glu	Val
335	340	345
Asp Gly Gly His Asn Lys Arg Trp Arg	Val Gly Val Cys Arg	Asp
350	355	360
Asp Val Asp Arg Arg Lys Glu Tyr Val	Thr Leu Ser Pro Asp	His
365	370	375
Gly Tyr Trp Val Leu Arg Leu Asn Gly	Glu His Leu Tyr Phe	Thr
380	385	390
Leu Asn Pro Arg Phe Ile Ser Val Phe	Pro Arg Thr Pro Pro	Thr
395	400	405
Lys Ile Gly Val Phe Leu Asp Tyr Glu	Cys Gly Thr Ile Ser	Phe
410	415	420
Phe Asn Ile Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Thr Cys	Arg
425	430	435
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	Glu Tyr Pro Ser Tyr	Asn
440	445	450
Glu Gln Asn Gly Thr Pro Ile Val Ile	Cys Pro Val Thr Gln	Glu
455	460	465
Ser Glu Lys Glu Ala Ser Trp Gln Arg	Ala Ser Ala Ile Pro	Glu
470	475	480
Thr Ser Asn Ser Glu Ser Ser Ser Gln	Ala Thr Thr Pro Phe	Leu
485	490	495
Pro Arg Gly Glu Met		
500		

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 149

gcgtggtcca cctctacagg gacg 24

<210> 150

<211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 150
ggaactgacc cagtgtgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 151
gcagatgcca cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggccttcctt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggaagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgccct gttgtgctgc gcgcgcgcgc ccgcgcgcgt cgcctcagcc 200
gcctcggcgg ggaatgtcac cggtgggcgc ggggcgcgcg ggcaggtgga 250
cgcgtcgcgc ggccccgggt tgcggggcga gccagaccac cccttccta 300
gggcgacggc tccacggcc caggccccga ggaccgggac ccgcgcgcgc 350
accgtccacc gacctctggc tgcgacttct ccagcccagt ccccgagac 400
caccctcttt tgggcgactg ctggaccctc ttccaccacc ttccaggcgc 450
cgctcggccc ctgcgcgacc accctccgcg cggcggaacg cacttcgacc 500
acctctcagg cgccgaccag acccgcgccg accaccttt cgacgaccac 550
tggccccggc cgaccaccc ctgtagcgac caccgtaccg gcgcccacga 600
ctccccggac ccgaccccc gatctcccca gcagcagcaa cagcagcgtc 650
ctccccaccc caactgcac cgaggccccc tcttcgcctc ctccagagta 700
tgtatgtaac tgctctgtgg ttggaagcct gaatgtgaat cgctgcaacc 750
agaccacagg gcagtgtgag tgtcggccag gttatcaggg gcttcactgt 800

gaaacctgca aagagggctt ttacctaaat tacacttctg ggctctgtca 850
 gccatgtgac tgtagtccac atggagctct cagcataccg tgcaacaggt 900
 aagcaacaga ggggtggaact gaagtttatt ttatttttagc aagggaaaaa 950
 aaaaggctgc tactctcaag gaccatactg gtttaaaca aggaggatga 1000
 gggcataga ttacaaaaat attttatata cttttattct cttactttat 1050
 atgttatatt taatgtcagg atttaaaaac atctaattta ctgatttagt 1100
 tcttcaaaag cactagagtc gccaatTTTT ctctgggata atttctgtaa 1150
 atttcatggg aaaaaattat tgaagaataa atctgctttc tggaagggt 1200
 ttcaggcatg aaacctgcta ggaggttag aaatgttctt atgtttatta 1250
 atataccatt ggagtttgag gaaatttggt gtttggttta ttttctctc 1300
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 ggtaccctaa tttatttaac tagtggaag tagactggtt ttactctatt 1400
 taccagtaca tttttgagac caaaagtaga ttaagcagga attatcttta 1450
 aactattatg ttatttgag gtaatttaat ctagtggaat aatgtactgt 1500
 tatctaagca ttgccttgt actgcactga aagtaattat tctttgacct 1550
 tatgtgaggc acttggttt ttgtggacc caagtcaaaa aactgaagag 1600
 acagtattaa ataatgaaaa aaataatgac aggttatact cagtgtaac 1650
 tgggtataac ccaagatctg ctgccactta cgagctgtgt tccttgggca 1700
 agtaatttcc tttcactgag cttgtttctt ctcaagggtt ttgtgaagat 1750
 taaatgagtt gatatatata aaatgcctag cacatgtcac tcaataaatt 1800
 ctggtttggt ttaatttcaa aggaatatta tggactgaaa tgagagaaca 1850
 tgttttaaga acttttagct ccttgacaaa gaagtgttt atactttagc 1900
 actaaatatt ttaaattgct tataaatgat attatactgt tatggaatat 1950
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000
 ctacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050
 tgaggccagg agttctagat gagcctggcc agcacagtga aacccgtct 2100
 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150
 tcccagctac tcgggaggct gaggcaggag aatcggttga acccgggagg 2200

tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250

agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys
1				5					10					15

Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn
				20					25					30

Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro
				35					40					45

Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala
				50					55					60

Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala
				65					70					75

Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro
				80					85					90

Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr
				95					100					105

Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala
				110					115					120

Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro
				125					130					135

Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val
				140					145					150

Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro
				155					160					165

Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro
				170					175					180

Ala	Thr	Glu	Ala	Pro	Ser	Ser	Pro	Pro	Pro	Glu	Tyr	Val	Cys	Asn
				185					190					195

Cys	Ser	Val	Val	Gly	Ser	Leu	Asn	Val	Asn	Arg	Cys	Asn	Gln	Thr
				200					205					210

Thr	Gly	Gln	Cys	Glu	Cys	Arg	Pro	Gly	Tyr	Gln	Gly	Leu	His	Cys
				215					220					225

Glu	Thr	Cys	Lys	Glu	Gly	Phe	Tyr	Leu	Asn	Tyr	Thr	Ser	Gly	Leu
				230					235					240

Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro
245 250 255

Cys Asn Arg

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 154

aactgctctg tggttggaag cctg 24

<210> 155

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 155

cagtcacatg gctgacagac ccac 24

<210> 156

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 156

aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157

<211> 689

<212> DNA

<213> Homo sapiens

<400> 157

tgcggcgcag tgtagacctg ggaggatggg cggcctgctg ctggctgctt 50

ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100

ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtaggcctc 150

ccgggaaaag ggctttgccca tggagaagga catgaagaac gtcgtggggg 200

tggtggtgac cctcaactcca gaaaacaacc tgcggacgct gtccctcag 250

cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300

ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350
 tgctggccac caacttcaga gactatgcca tcattctcac tcagctggag 400
 ttccggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gaggccatgg ggctcttcac caagtggagc aggagcctgg 500
 gcttctgtgc acagtagcag gccagctgc agaaggacct cacctgtgct 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
 gggctctgtg acctcgcca gtgtccaccc acctcgctca ggggtctccg 650
 gggcccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90
 Arg Asn Ser Gly Trp Val Phe Glu Asn Pro Ser Ile Gly Val Leu
 95 100 105
 Glu Leu Trp Val Leu Ala Thr Asn Phe Arg Asp Tyr Ala Ile Ile
 110 115 120
 Phe Thr Gln Leu Glu Phe Gly Asp Glu Pro Phe Asn Thr Val Glu
 125 130 135
 Leu Tyr Ser Leu Thr Glu Thr Ala Ser Gln Glu Ala Met Gly Leu
 140 145 150
 Phe Thr Lys Trp Ser Arg Ser Leu Gly Phe Leu Ser Gln
 155 160

<210> 159

<211> 1665
<212> DNA
<213> Homo sapiens

1400 > 159
aapagacgtt cctcgcggc cctggcacct ctaaccccag acatgctgct 50
gctgctgctg ccctgctct gggggaggga gagggcggaa ggacagacaa 100
gtaaactgct gacgatgcag agttccgtga cggcgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccacccc tcgcatggct ggatttacc 200
tggcccagta gttcatggct actggttccg ggaaggggccc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctcgggcagt gtgggaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcacc agagatgcc aagaagtga tgcggggaga tacttttttc 400
gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450
gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550
gtgagcaggg gacaccccct atgatctcct ggatagggac ctccgtgtcc 600
ccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650
gcccaggac catggcacca gcctcacctg tcaggtgacc ttccctggg 700
ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctaccgcct 750
cagaacttga ccatgactgt ctccaagga gacggcacag tatccacagt 800
cttgggaaat ggtcatctc tgtcactccc agagggccag tctctgcgc 850
tggctctgtc agttgatgca gttgacagca atccccctgc caggctgagc 900
ctgagctgga gaggcctgac cctgtgcccc tcacagccct caaacccggg 950
ggctgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000
gcagagctca gaacctctc ggctctcagc aggtctacct gaacgtctcc 1050
ctgcagagca aagccacatc aggagtgact caggggggtg tcgggggagc 1100
tggagccaca gccctggtct tctgtcctt ctgcgtcacc ttcggtgtag 1150
tgaggctctg caggaagaaa tcggcaaggc cagcagcggg cgtgggagat 1200
acgggcatag aggatgcaaa cgctgtcagg ggttcagcct ctacggggcc 1250
cctgactgaa ccttgggcag aagacagtcc ccagaccag cctccccag 1300

cttctgcccg ctctcagtg ggggaaggag agctccagta tgcattccctc 1350
 agcttccaga tggtaagcc ttgggactcg cggggacagg aggccactga 1400
 caccgagtac tcggagatca agatccacag atgagaaaact gcagagactc 1450
 accctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataacact 1550
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgcctccct tttatttttt taactaaaag 1650
 acagacaaat tccta 1665

<210> 160
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala
 1 5 10 15
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
 20 25 30
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
 50 55 60
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
 65 70 75
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
 80 85 90
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
 95 100 105
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg
 110 115 120
 Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu
 125 130 135
 Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile
 140 145 150
 Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser
 155 160 165
 Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp
 170 175 180

Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405
Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala	410	415	420
Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser	425	430	435
Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu	440	445	450
Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg	455	460	

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgcccagt gacctgccga ggtcggcagc acagagctct ggagatgaag 50
 acctgtttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagtg 200
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250
 gagggaggat cgggtgatcc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atagagcgc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccga ggaaggacca ctacatcttt tactgcaaag accagcacca 400
 tggggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
 accgggaggc cctggaagaa tttaagaaat tgggtgcagc caagggactc 500
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550
 aactaggca gcccccgggt ctgcacctcc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctaccc tccagccatg acctttccct 650
 gctccacccc acctgactcc aaataaagtc cttttccccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr
 20 25 30
 Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg
 35 40 45
 Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly
 50 55 60
 Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile
 65 70 75

Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr	
				80					85					90	
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro	
				95					100					105	
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly	
				110					115					120	
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr	
				125					130					135	
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys	
				140					145					150	
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser	
				155					160					165	
Cys	Val	Pro	Glu	His											
				170											

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 165
 gtccctccgga aagtccttat c 21

<210> 166
 <211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 166
gactagtgtt cgggaacgca gcttc 25

<210> 167
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 167
cagggacgtg gtacgtgaag gccatggtgg tcgataagga ctttcaggag 50

<210> 168
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 168
ctgtccttca ccttgaggga ggaggatgc acagggacgt ggtac 45

<210> 169
<211> 1204
<212> DNA
<213> Homo sapiens

<400> 169
gttcgcgaga tgcagaggtt gaggtgggtg cgggaactgga agtcacggg 50
cagaggtctc acagcagaca aggaacgttg ggcccgctcc tccccctccc 100
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150
gtagggggag agaccaggat catcaagggg ttcgagtgcg agcctcaact 200
ccagcccttg caggcagccc tgttcgagaa gacgggcta ctctgtgggg 250
cgacgtcat cgcgcccgaga tggctcctga cagcagccca ctgcctcaag 300
ccccgtaca tagttcacct ggggcagcac aacctcaga aggaggaggg 350
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acaacagcct ccccaacaaa gaccacgca atgacatcat gctgggtgaag 450
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 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

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				20					25					30
His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Phe	Glu	Lys	Thr	Arg	Leu
				35					40					45
Leu	Cys	Gly	Ala	Thr	Leu	Ile	Ala	Pro	Arg	Trp	Leu	Leu	Thr	Ala
				50					55					60
Ala	His	Cys	Leu	Lys	Pro	Arg	Tyr	Ile	Val	His	Leu	Gly	Gln	His
				65					70					75
Asn	Leu	Gln	Lys	Glu	Glu	Gly	Cys	Glu	Gln	Thr	Arg	Thr	Ala	Thr
				80					85					90
Glu	Ser	Phe	Pro	His	Pro	Gly	Phe	Asn	Asn	Ser	Leu	Pro	Asn	Lys
				95					100					105

Asp His Arg Asn Asp Ile Met Leu Val	Lys Met Ala Ser Pro Val
110	115 120
Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys	
125	130 135
Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr	
140	145 150
Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn	
155	160 165
Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly	
170	175 180
Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly	
185	190 195
Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn	
200	205 210
Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala	
215	220 225
Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val	
230	235 240
Asp Trp Ile Gln Glu Thr Met Lys Asn Asn	
245	250

<210> 171
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 171
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<210> 172
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 172
 ctccaggcca tgaggattct gcag 24

<210> 173
 <211> 18
 <212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 173
tctctgggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
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<220>
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<400> 174
tctgtgatgt tgcgggggta ggcg 24

<210> 175
<211> 25
<212> DNA
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<220>
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<400> 175
cgtgtagaca ccaggcttgc gggtg 25

<210> 176
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 176
cccttgatga tcctggtc 18

<210> 177
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 177
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
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<400> 178
gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179
<211> 907
<212> DNA
<213> Homo sapiens

<400> 179
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aagaaagagg agagcaccga agaagtgaat atagaagttt tgcacgtcc 150
agaaaactgc tctaagacaa gcaagaaggg agacctaata aatgcccatt 200
atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250
caaatgaag gccaccccaa atggtttggt cttgggtgtg ggcaagtcac 300
aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350
aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400
ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450
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acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550
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tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650
ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700
atttctactt ttttttttta gctatttact gtactttatg tataaaacaa 750
agtcactttt ctccaagttg tatttgctat tttcccta tgagaagata 800
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ttgcaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaa 907

<210> 180
<211> 222
<212> PRT
<213> Homo sapiens

<400> 180
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				20					25					30	
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn	
				35					40					45	
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr	
				50					55					60	
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg	
				65					70					75	
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly	
				80					85					90	
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro	
				95					100					105	
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly	
				110					115					120	
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu	
				125					130					135	
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser	
				140					145					150	
Ile	Glu	Thr	Phe	Lys	Gln	Ile	Asp	Met	Asp	Asn	Asp	Arg	Gln	Leu	
				155					160					165	
Ser	Lys	Ala	Glu	Ile	Asn	Leu	Tyr	Leu	Gln	Arg	Glu	Phe	Glu	Lys	
				170					175					180	
Asp	Glu	Lys	Pro	Arg	Asp	Lys	Ser	Tyr	Gln	Asp	Ala	Val	Leu	Glu	
				185					190					195	
Asp	Ile	Phe	Lys	Lys	Asn	Asp	His	Asp	Gly	Asp	Gly	Phe	Ile	Ser	
				200					205					210	
Pro	Lys	Glu	Tyr	Asn	Val	Tyr	Gln	His	Asp	Glu	Leu				
				215					220						

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 181

gtgttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 182
gacatggaca atgacagg 18

<210> 183
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 183
ccttttcagga tgtaggag 18

<210> 184
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 184
gatgtctgcc accccaag 18

<210> 185
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcacctgat atgacttgtc acgtggc 27

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
tacaagaggg aagaggagtt gcac 24

<210> 187
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 187

gcccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50

cc 52

<210> 188

<211> 573

<212> DNA

<213> Homo sapiens

<400> 188

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cccaaatgct tctgtgtca ataactca ctgcacctgc aacctggat 150

atacttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200

aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250

aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300

atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350

ggtgcatgcc tgcaatccca gttactcggg aggetgaggc aggagaatcg 400

cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450

ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500

ttcttgtttc atttcgcgac tgccctctca gtgtttctctg ggatccccctc 550

ccaaataaag tacttatatt ctc 573

<210> 189

<211> 74

<212> PRT

<213> Homo sapiens

<400> 189

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Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
20 25 30

Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
35 40 45

Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
50 55 60

Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
65 70

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 190
agggaccatt gcttcttcca ggcc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 191
cgttacatgt ctccaagggg aatg 24

<210> 192
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 192
ctgtgctaa gtgccccca aatgcttctt gtgtcaataa cactcactgc 50

<210> 193
<211> 1091
<212> DNA
<213> Homo sapiens

<400> 193
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gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
gctcactgca gcggcagcag gtactgggtg cgctggggg aacacagcct 350
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cccatcccg ctaactggga gcctcgacga gccacgagca cgacctccgg 450

ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccctt 500
 gccctgccc aatgactgtg caaccgctgg caccgagtgc cacgtctcag 550
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 ccctagctcc actcttggtg gcctgggaac ttcttggaa tttaactcct 1000
 gccagccctt ctaagacca cgagcggggg gagagaagtg tgcaatagtc 1050
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194

<211> 248

<212> PRT

<213> Homo sapiens

<400> 194

Met	Gly	Leu	Ser	Ile	Phe	Leu	Leu	Leu	Cys	Val	Leu	Gly	Leu	Ser	1	5	10	15
Gln	Ala	Ala	Thr	Pro	Lys	Ile	Phe	Asn	Gly	Thr	Glu	Cys	Gly	Arg	20	25	30	
Asn	Ser	Gln	Pro	Trp	Gln	Val	Gly	Leu	Phe	Glu	Gly	Thr	Ser	Leu	35	40	45	
Arg	Cys	Gly	Gly	Val	Leu	Ile	Asp	His	Arg	Trp	Val	Leu	Thr	Ala	50	55	60	
Ala	His	Cys	Ser	Gly	Ser	Arg	Tyr	Trp	Val	Arg	Leu	Gly	Glu	His	65	70	75	
Ser	Leu	Ser	Gln	Leu	Asp	Trp	Thr	Glu	Gln	Ile	Arg	His	Ser	Gly	80	85	90	
Phe	Ser	Val	Thr	His	Pro	Gly	Tyr	Leu	Gly	Ala	Ser	Thr	Ser	His	95	100	105	
Glu	His	Asp	Leu	Arg	Leu	Leu	Arg	Leu	Arg	Leu	Pro	Val	Arg	Val	110	115	120	

Thr	Ser	Ser	Val	Gln	Pro	Leu	Pro	Leu	Pro	Asn	Asp	Cys	Ala	Thr	125	130	135
Ala	Gly	Thr	Glu	Cys	His	Val	Ser	Gly	Trp	Gly	Ile	Thr	Asn	His	140	145	150
Pro	Arg	Asn	Pro	Phe	Pro	Asp	Leu	Leu	Gln	Cys	Leu	Asn	Leu	Ser	155	160	165
Ile	Val	Ser	His	Ala	Thr	Cys	His	Gly	Val	Tyr	Pro	Gly	Arg	Ile	170	175	180
Thr	Ser	Asn	Met	Val	Cys	Ala	Gly	Gly	Val	Pro	Gly	Gln	Asp	Ala	185	190	195
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gly	Gly	Val	Leu	200	205	210
Gln	Gly	Leu	Val	Ser	Trp	Gly	Ser	Val	Gly	Pro	Cys	Gly	Gln	Asp	215	220	225
Gly	Ile	Pro	Gly	Val	Tyr	Thr	Tyr	Ile	Cys	Lys	Tyr	Val	Asp	Trp	230	235	240
Ile	Arg	Met	Ile	Met	Arg	Asn	Asn								245		

<210> 195

<211> 1485

<212> DNA

<213> Homo sapiens

<400> 195

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tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300
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 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Hcno sapiens

<400> 196

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Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn	30
				20					25						
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu	45
				35					40						
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp	60
				50					55						
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met	75
				65					70						

Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
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 <211> 4842
 <212> DNA
 <213> Homo sapiens

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<211> 1523

<212> PFT

<213> Hcmo sapiens

<400> 198

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Leu	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Ser	Val	Leu	Ser	Gly	Pro	Pro
					20				25				30	

Ala	Val	Ala	Cys	Pro	Thr	Lys	Cys	Thr	Cys	Ser	Ala	Ala	Ser	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35	40	45
Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro	50	55 60
Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg	65	70 75
Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu	80	85 90
His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe	95	100 105
Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys	110	115 120
Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu	125	130 135
Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg	140	145 150
Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp	155	160 165
Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175 180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Ile Ser Arg	185	190 195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205 210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220 225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235 240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250 255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265 270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280 285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295 300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310 315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr		

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Lys Lys Leu Lys Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser	Leu
350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu Phe	
365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn Lys	
380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn Leu	
395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser Lys	
410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile	Gln Thr Leu His Leu Ala	
425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His	Leu Lys Trp Leu Ala Asp	
440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys Ser	
455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser	
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe	
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg	
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg	
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn	
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys	
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys	
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu	
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val	
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn	

605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser	
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr	
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu	
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly	
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys	
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala	
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln	
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val	
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met	
740	745	750
Pro Lys Asp Val Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu Thr	
755	760	765
Ala Val Pro Arg Glu Leu Ser Ala Leu	Arg His Leu Thr Leu Ile	
770	775	780
Asp Leu Ser Asn Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr Phe	
785	790	795
Ser Asn Met Ser His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn Arg	
800	805	810
Leu Arg Cys Ile Pro Val His Ala Phe	Asn Gly Leu Arg Ser Leu	
815	820	825
Arg Val Leu Thr Leu His Gly Asn Asp	Ile Ser Ser Val Pro Glu	
830	835	840
Gly Ser Phe Asn Asp Leu Thr Ser Leu	Ser His Leu Ala Leu Gly	
845	850	855
Thr Asn Pro Leu His Cys Asp Cys Ser	Leu Arg Trp Leu Ser Glu	
860	865	870
Trp Val Lys Ala Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys Ser	
875	880	885
Ser Pro Glu Pro Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro Thr	

890	895	900
His Arg Phe Gln Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
905	910	915
Lys Cys Asn Ala Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
920	925	930
Cys Thr Gln Asp Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
935	940	945
Ser Tyr Lys Gly Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
950	955	960
Gln Asn Pro Cys Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
965	970	975
His Lys Asp Gly Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
980	985	990
Gln Arg Cys Glu Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
995	1000	1005
Glu Asn Asn Ala Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
1010	1015	1020
Ile Cys Pro Pro Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
1025	1030	1035
Asp His Cys Val Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys
1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser	Cys Glu Cys Val Pro	Gly
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp	Asn Asp Asp Cys Val	Ala
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys	Val Asp Thr Ile Asn	Gly
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe	Ser Gly Pro Phe Cys	Glu
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln	Thr Ser Pro Cys Asp	Gln
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys	Ile Val Val Gln Gln	Glu
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe	Ala Gly Pro Arg Cys	Glu
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly	Lys Asp Ser Tyr Val	Glu
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln	Ala Asn Ile Ser Leu	Gln

1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335
Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser		
1340	1345	1350
Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp		
1355	1360	1365
Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly		
1370	1375	1380
Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu		
1385	1390	1395
Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn		
1400	1405	1410
Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser		
1415	1420	1425
Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly		
1430	1435	1440
Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg		
1445	1450	1455
Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala		

1460	1465	1470
Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln		
1475	1480	1485
Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln		
1490	1495	1500
Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu		
1505	1510	1515
Glu Cys Gly Cys Leu Ala Cys Ser		
1520		

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 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 200
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 200
 ttgttgcat tgaggaggag cagc 24

<210> 201
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 201
 gagggcatcg togaaatacg cctagaacag aactccatca aagccatccc 50

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<210> 203

<211> 148

<212> PRT

<213> Homo sapiens

<400> 203

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Gly	Ala	Glu	Ser	Lys	Ile	Tyr	Thr	Arg	Cys	Lys	Leu	Ala	Lys	Ile	30
				20					25						
Phe	Ser	Arg	Ala	Gly	Leu	Asp	Asn	Tyr	Trp	Gly	Phe	Ser	Leu	Gly	45
				35					40						
Asn	Trp	Ile	Cys	Met	Ala	Tyr	Tyr	Glu	Ser	Gly	Tyr	Asn	Thr	Thr	60
				50					55						
Ala	Pro	Thr	Val	Leu	Asp	Asp	Gly	Ser	Ile	Asp	Tyr	Gly	Ile	Phe	75
				65					70						
Gln	Ile	Asn	Ser	Phe	Ala	Trp	Cys	Arg	Arg	Gly	Lys	Leu	Lys	Glu	90
				80					85						
Asn	Asn	His	Cys	His	Val	Ala	Cys	Ser	Ala	Leu	Ile	Thr	Asp	Asp	105
				95					100						
Leu	Thr	Asp	Ala	Ile	Ile	Cys	Ala	Arg	Lys	Ile	Val	Lys	Glu	Thr	120
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Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
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Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
140 145

<210> 204

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 204

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<210> 205

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 205

ctcattggct gcctggtcac aggc 24

<210> 206

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 206

ccagtcggac aggtctctcc cctc 24

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<223> Synthetic oligonucleotide probe

<400> 207

tcagtgacca aggctgagca ggcg 24

<210> 208

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 208

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<210> 209

<211> 1648

<212> DNA

<213> Homo sapiens

<400> 209

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 <212> PRT
 <213> Homo sapiens

<400> 210
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 20 25 30
 Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
 35 40 45
 Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
 50 55 60
 Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
 65 70 75
 Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
 80 85 90
 Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
 95 100 105
 Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
 110 115 120
 Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
 125 130 135
 Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
 140 145 150
 Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp

155	160	165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg		
170	175	180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val		
185	190	195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe		
200	205	210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val		
215	220	225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu		
230	235	240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly		
245	250	255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu		
260	265	270
Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg		
275	280	285
Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg		
290	295	300
Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr		
305	310	315
Arg Tyr Val Thr Lys Leu Leu Val		
320		

<210> 211

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 211

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cttcgcgata ttccgccgta ccttcttgct ggcgttggtg ggagccgtgc 100

tctacctata tccggcttcc agacaagctg caggaattcc agggattact 150

ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200

tttgcgatgag ttcttggtta atttgcata gagatatggg cctgtggtct 250

ccttctggtt tggcaggcgc ctcttggtta gtttgggcac tgttgatgta 300

ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350

gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaaa 400

accacatgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
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 gctctctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550
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 agcttggate actgtctcaa agagatatta aaattttata catttaaaat 1450
 cattgttaaa ttgattgagg aaaacaacca tttaaaaaaa atctatgttg 1500
 aatcctttta taaaccagta tcactttgta atataaacac ctatttgtac 1550
 ttaa 1554

<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
1					5				10					15

Val Gly Ala Val	Leu Tyr Leu Tyr Pro	Ala Ser Arg Gln Ala Ala	20	25	30
Gly Ile Pro Gly Ile	Thr Pro Thr Glu Glu Lys Asp Gly Asn Leu		35	40	45
Pro Asp Ile Val Asn Ser Gly Ser Leu His Glu Phe Leu Val Asn			50	55	60
Leu His Glu Arg Tyr Gly Pro Val Val Ser Phe Trp Phe Gly Arg			65	70	75
Arg Leu Val Val Ser Leu Gly Thr Val Asp Val Leu Lys Gln His			80	85	90
Ile Asn Pro Asn Lys Thr Ser Asp Pro Phe Glu Thr Met Leu Lys			95	100	105
Ser Leu Leu Arg Tyr Gln Ser Gly Gly Gly Ser Val Ser Glu Asn			110	115	120
His Met Arg Lys Lys Leu Tyr Glu Asn Gly Val Thr Asp Ser Leu			125	130	135
Lys Ser Asn Phe Ala Leu Leu Leu Lys Leu Ser Glu Glu Leu Leu			140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser			155	160	165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val			170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln			185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu			200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu			215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys			230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser			245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser			260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys			275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys			290	295	300

Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val
 305 310 315
 Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu
 320 325 330
 Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln
 335 340 345
 Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg
 350 355 360
 Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro
 365 370 375
 Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp
 380 385 390
 Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly
 395 400 405
 Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr
 410 415 420
 Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val
 425 430 435
 Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450
 Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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 tcagggcttg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150
 cgtcatcacc ttattctggt cccgggacag caacatacag gctgcctgc 200
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250
 gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccggttt 300
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350
 gggctcactg tagtgcaccc gtggccctgt ccttcttcat attcgagcgt 400
 tgggagtgca ctacgtattg gtacattttt gtcttctgca gtgcccttcc 450

agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcgggt 600
 ttcccctcgg aaactgcttc tgctggagga tatgtgttgg aataattacg 650
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700
 tgtttttag tagtaacattaag acttatatac agtttttaggg gacaattaa 750
 aaaaaaaaa 759

<210> 214
 <211> 140
 <212> PRT
 <213> Homo sapiens

<400> 214
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu 15
 1 5 10
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp 30
 20 25
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu 45
 35 40
 Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr 60
 50 55
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val 75
 65 70
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His 90
 80 85
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp 105
 95 100
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu 120
 110 115
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu 135
 125 130
 Lys Lys Lys Pro Phe 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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cctgggtctt ccccgacctt cttcgactcg gagcggtctt ggagacagaa 100
 gaccgggctt gctgcagccc catagtcccc cggaacgagt ggaaggccct 150
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200
 tatcgcacac ggcgggcagc agctgcaaca ccccgacctt gtgccagcag 250
 caggccccga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300
 cgtgggctac aacttcttga ttggagaaga cgggctcgta tacgagggcc 350
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400
 tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450
 ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500
 gagccctgag gtccaactat gtgctcaaag gacaccggga tgtgcagcgt 550
 aactctctc caggcaacca gctctaccac ctcattccaga attggccaca 600
 ctaccgctcc cctgaggccc ctgctgatcc gcacccatt cctccctcc 650
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216

<211> 196

<212> PRT

<213> Homo sapiens

<400> 216

Met	Ser	Arg	Arg	Ser	Met	Leu	Leu	Ala	Trp	Ala	Leu	Pro	Ser	Leu	
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Leu	Arg	Leu	Gly	Ala	Ala	Gln	Glu	Thr	Glu	Asp	Pro	Ala	Cys	Cys	
			20						25					30	
Ser	Pro	Ile	Val	Pro	Arg	Asn	Glu	Trp	Lys	Ala	Leu	Ala	Ser	Glu	
				35					40					45	
Cys	Ala	Gln	His	Leu	Ser	Leu	Pro	Leu	Arg	Tyr	Val	Val	Val	Ser	
				50					55					60	
His	Thr	Ala	Gly	Ser	Ser	Cys	Asn	Thr	Pro	Ala	Ser	Cys	Gln	Gln	
				65					70					75	
Gln	Ala	Arg	Asn	Val	Gln	His	Tyr	His	Met	Lys	Thr	Leu	Gly	Trp	
				80					85					90	
Cys	Asp	Val	Gly	Tyr	Asn	Phe	Leu	Ile	Gly	Glu	Asp	Gly	Leu	Val	
				95					100					105	
Tyr	Glu	Gly	Arg	Gly	Trp	Asn	Phe	Thr	Gly	Ala	His	Ser	Gly	His	
				110					115					120	

Leu	Trp	Asn	Pro	Met	Ser	Ile	Gly	Ile	Ser	Phe	Met	Gly	Asn	Tyr
				125					130					135
Met	Asp	Arg	Val	Pro	Thr	Pro	Gln	Ala	Ile	Arg	Ala	Ala	Gln	Gly
				140					145					150
Leu	Leu	Ala	Cys	Gly	Val	Ala	Gln	Gly	Ala	Leu	Arg	Ser	Asn	Tyr
				155					160					165
Val	Leu	Lys	Gly	His	Arg	Asp	Val	Gln	Arg	Thr	Leu	Ser	Pro	Gly
				170					175					180
Asn	Gln	Leu	Tyr	His	Leu	Ile	Gln	Asn	Trp	Pro	His	Tyr	Arg	Ser
				185					190					195

Pro

<210> 217
 <211> 1871
 <212> LNA
 <213> Homo sapiens

<400> 217
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 tctatctggt catctgtggc caggatgatg gtcctcccg ctcagaggac 150
 cctgagcgtg atgaccacga gggccagccc cggccccggg tgccctggaa 200
 gcgggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250
 tagggctgct ggccccgctt ggggaggctt ggggcattct tgggcagccc 300
 cccaaccgcc cgaaccacag cccccaccc tcagccaagg tgaagaaaat 350
 ctttggtctg ggcgacttct actccaacat caagacggtg gccctgaacc 400
 tgctcgtcac agggaagatt gtggaccatg gcaatgggac cttcagcgtc 450
 cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500
 gccccccagt aaagctgtag agttccacca ggaacagcag atcttcacg 550
 aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600
 gaacggggcc gccggacctc gctttgcacc cagacccag ccaagatctg 650
 ctcccagac cagctcaga gctcagccac ctggagctgc tcccagccct 700
 tcaaagtcgt ctgtgtctac atgccttct acagcacgga ctatcggctg 750
 gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800
 cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850

ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaagg 900
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 aataaagctt gccccggggc a 1871

<210> 218

<211> 252

<212> PRT

<213> Homo sapiens

<400> 218

Met	Gln	Leu	Thr	Arg	Cys	Cys	Phe	Val	Phe	Leu	Val	Gln	Gly	Ser
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Leu	Tyr	Leu	Val	Ile	Cys	Gly	Gln	Asp	Asp	Gly	Pro	Pro	Gly	Ser
				20				25						30

Glu	Asp	Pro	Glu	Arg	Asp	Asp	His	Glu	Gly	Gln	Pro	Arg	Pro	Arg
				35					40					45

Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50 55 60
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80 85 90
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
 110 115 120
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
 125 130 135
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
 140 145 150
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
 155 160 165
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
 170 175 180
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
 185 190 195
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
 200 205 210
 Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225
 Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240
 Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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 gcaggggccc caggcagggc tgattcttgg gcggaggaga gtagggtaaa 100
 gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150
 agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200

gcgcgcgcgc cgcgcgcgc cctgcagcgc tgcgcaccta gccgctagca 250
 tcttcccagag caccgggata ccggggtagg aggcgacgcg ggcgagcacc 300
 agcgcagcc ggctgcggct gccacacgg ctcaccatgg gctccgggcg 350
 ccgggcgcctg tccgcgggtgc cggccgtgct gctggctctc acgctgccgg 400
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 aagacgcgca tcatttactt cgatcagatc ctgggtgaatg tgggtaattt 650
 tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700
 tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750
 ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800
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 cgtagacatg accactttat taactgggtg tgggatgctg ttgtttctaa 1850
 ttatacctat ttttcaaggc ttctgttgta tttgaagtat catctgggtt 1900
 tgccttaact ctttaaattg tatatattta tctgttttagc taatattaa 1950
 ttcaaatac ccatacttaa atttagtgca atatcttgtc ttttgtatag 2000
 gtcatatgaa ttcataaaat tatttatgtc tggtatagaa taaagattaa 2050
 tatatgttaa aaaaa 2065

<210> 220
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 220
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 Leu Val Leu Thr Leu Pro Gly Leu Pro Val Trp Ala Gln Asn Asp
 20 25 30
 Thr Glu Pro Ile Val Leu Glu Gly Lys Cys Leu Val Val Cys Asp
 35 40 45
 Ser Asn Pro Ala Thr Asp Ser Lys Gly Ser Ser Ser Ser Pro Leu
 50 55 60
 Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala
 65 70 75
 Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr
 80 85 90
 Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe
 95 100 105
 Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr
 110 115 120
 Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile
 125 130 135
 Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe
 140 145 150
 Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val
 155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu
 170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly
 185 190 195

Phe Leu Val Phe Pro Leu
 200

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 221
 acggctcacc atgggctccg 20

<210> 222
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 222
 aggaagagga gcccttgag tccg 24

<210> 223
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 223
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<210> 224
 <211> 902
 <212> DNA
 <213> Homo sapiens

<400> 224
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 tatcatcttc ctcatcgccg gagctttctt ctggttggtg tctctactga 150
 ttctgctcct tgtttggttc atggcaagag tcattattga caacaaagat 200

ggaccaaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250
 tatccaagaa atgttccgat ttgcatatta taaactotta aaaaaagcca 300
 gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350
 ctgctggcct atgtttctgg cttgggcttt ggaatcatga gtggagtatt 400
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 ttcattgaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500
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 tgagaagaaa aagtggggca tcctccttat cgttctcctg acccactgc 600
 tgggtgcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650
 tcagcattta taatcctggg gtcctgggc acctgggcat tcttagctgc 700
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ta 902

<210> 225

<211> 257

<212> PFT

<213> Homo sapiens

<400> 225

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Pro	Ala	Leu	Ala	Leu	Tyr	Val	Phe	Thr	Ile	Ala	Ile	Glu	Pro	Leu	30
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Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	45
				35					40						
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	60
				50					55						
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	75
				65					70						
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	90
				80					85						
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	105
				95					100						

Pro Gly Glu Thr Ala Pro Ser Met Arg	Leu Leu Ala Tyr Val Ser	110	115	120
Gly Leu Gly Phe Gly Ile Met Ser Gly	Val Phe Ser Phe Val Asn	125	130	135
Thr Leu Ser Asp Ser Leu Gly Pro Gly	Thr Val Gly Ile His Gly	140	145	150
Asp Ser Pro Gln Phe Phe Leu Tyr Ser	Ala Phe Met Thr Leu Val	155	160	165
Ile Ile Leu Leu His Val Phe Trp Gly	Ile Val Phe Phe Asp Gly	170	175	180
Cys Glu Lys Lys Lys Trp Gly Ile Leu	Leu Ile Val Leu Leu Thr	185	190	195
His Leu Leu Val Ser Ala Gln Thr Phe	Ile Ser Ser Tyr Tyr Gly	200	205	210
Ile Asn Leu Ala Ser Ala Phe Ile Ile	Leu Val Leu Met Gly Thr	215	220	225
Trp Ala Phe Leu Ala Ala Gly Gly Ser	Cys Arg Ser Leu Lys Leu	230	235	240
Cys Leu Leu Cys Gln Asp Lys Asn Phe	Leu Leu Tyr Asn Gln Arg	245	250	255

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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser	35	40	45	
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn	50	55	60	
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75	
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90	
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105	
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120	
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser				

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185	190	195
Pro Cys Ser Val Ile Ser Ile Gln Asp Val Leu Cys Pro Val Tyr		
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Asp Leu Asp Asn Asn Val Ala Phe Ile Gly Met Tyr Gln Thr Met		
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Thr Lys Lys Ala Ala Ile Thr Val Gln Arg Lys Asp Phe Pro Ser		
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Cys Gly Gly Ser Leu Pro Phe Tyr Pro Phe Ala Glu Asp Glu Pro		
260	265	270
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Gln Ala Val Thr Ser Glu Ala Tyr Val Ser Gly Met Leu Phe Cys		
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Leu Gly Ile Phe Leu Ser Phe Tyr Leu Leu Thr Val Leu Leu Ala		
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Cys Trp Glu Asn Trp Arg Gln Lys Lys Lys Thr Leu Leu Val Ala		
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Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala		
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470	475	480
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485	490	495
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635	640	645
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Asp Ser Gly Ile Phe Arg Arg Ile Leu	His Val Leu Tyr Thr	Asp
665	670	675
Cys Ile Arg Gln Cys Ser Gly Pro Leu	Tyr Val Asp Arg Met	Val
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Leu Leu Val Met Gly Asn Val Ile Asn	Trp Ser Leu Ala Ala	Tyr

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				740					745					750					
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe					
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Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser					
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Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp					
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His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser					
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Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln					
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<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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 50 55 60
 Ser Gly Lys Ala Thr Glu Gly Pro Phe Ala Met Asp Pro Asp Ser
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 Gly Phe Leu Leu Val Thr Arg Ala Leu Asp Arg Glu Glu Gln Ala

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110	115	
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125	130	
Ser Arg Gly Thr Arg Pro Gly Ile Pro	Phe Leu Phe Leu Glu Ala	150
140	145	
Ser Asp Arg Asp Glu Pro Gly Thr Ala	Asn Ser Asp Leu Arg Phe	165
155	160	
His Ile Leu Ser Gln Ala Pro Ala Gln	Pro Ser Pro Asp Met Phe	180
170	175	
Gln Leu Glu Pro Arg Leu Gly Ala Leu	Ala Leu Ser Pro Lys Gly	195
185	190	
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His Leu Glu Ser His Pro Pro Gly Pro	Phe Glu Val Asn Ala Glu	285
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Gly Asn Leu Tyr Val Thr Arg Glu Leu	Asp Arg Glu Ala Gln Ala	300
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Glu Tyr Leu Leu Gln Val Arg Ala Gln	Asn Ser His Gly Glu Asp	315
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Asp Asn Val Pro Ile Cys Pro Pro Arg	Asp Pro Thr Val Ser Ile	345
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Pro Glu Leu Ser Pro Pro Gly Thr Glu	Val Thr Arg Leu Ser Ala	360
350	355	
Glu Asp Ala Asp Ala Pro Gly Ser Pro	Asn Ser His Val Val Tyr	

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Phe Gln Val Asp Pro Thr Ser Gly Ser Val Thr Leu Gly Val Leu	395	400	405
Pro Leu Arg Ala Gly Gln Asn Ile Leu Leu Leu Val Leu Ala Met	410	415	420
Asp Leu Ala Gly Ala Glu Gly Gly Phe Ser Ser Thr Cys Glu Val	425	430	435
Glu Val Ala Val Thr Asp Ile Asn Asp His Ala Pro Glu Phe Ile	440	445	450
Thr Ser Gln Ile Gly Pro Ile Ser Leu Pro Glu Asp Val Glu Pro	455	460	465
Gly Thr Leu Val Ala Met Leu Thr Ala Ile Asp Ala Asp Leu Glu	470	475	480
Pro Ala Phe Arg Leu Met Asp Phe Ala Ile Glu Arg Gly Asp Thr	485	490	495
Glu Gly Thr Phe Gly Leu Asp Trp Glu Pro Asp Ser Gly His Val	500	505	510
Arg Leu Arg Leu Cys Lys Asn Leu Ser Tyr Glu Ala Ala Pro Ser	515	520	525
His Glu Val Val Val Val Val Gln Ser Val Ala Lys Leu Val Gly	530	535	540
Pro Gly Pro Gly Pro Gly Ala Thr Ala Thr Val Thr Val Leu Val	545	550	555
Glu Arg Val Met Pro Pro Pro Lys Leu Asp Gln Glu Ser Tyr Glu	560	565	570
Ala Ser Val Pro Ile Ser Ala Pro Ala Gly Ser Phe Leu Leu Thr	575	580	585
Ile Gln Pro Ser Asp Pro Ile Ser Arg Thr Leu Arg Phe Ser Leu	590	595	600
Val Asn Asp Ser Glu Gly Trp Leu Cys Ile Glu Lys Phe Ser Gly	605	610	615
Glu Val His Thr Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp	620	625	630
Thr Tyr Thr Val Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu	635	640	645
Ala Pro Val Pro Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His			

650	655	660
Gly Leu Ile Val Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
665	670	675
Gly His Gly Pro Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
680	685	690
Gln Arg Asp Trp Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
695	700	705
Leu Thr Leu Ala Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
710	715	720
Pro Val Val Val Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
725	730	735
Arg Val Ile Val Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
740	745	750
Lys Val Gly Arg Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
755	760	765
Gly Ile Leu Val Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
770	775	780
Leu Ile Phe Thr His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
785	790	795
Gln Pro Ala Asp Ser Val Pro Leu Lys Ala Thr Val		
800	805	

<110> 230
 <111> 50
 <112> DNA
 <113> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 230
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<210> 231
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 231
 cctgagctgt aaccccaactc cagg 24

<210> 232
 <211> 23
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

agagtctgtc ccagctatct tgt 23

<210> 233

<211> 2786

<212> DNA

<213> Homo sapiens

<400> 233

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cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150
acttgaagct caatttcttg aaatctccct cctccttcaa tgggctgtg 200
gatgtcctgg tcccatctgt cagtctgcag gcatttaaact ccttctgtg 250
atccagggc ttagagtacg cagtgcacat tgaggacctg caggcccttt 300
tagacaatga agatgatgaa atgcaacaca atgaagggca agaacggagc 350
agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400
cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450
agattggaca ttctttgaa aaccggccga tgtatgtact gaagttcagc 500
actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550
ttcccgagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600
ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650
atggatattt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700
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gtcctgcac tgggtgctgac ccaaatagaa actggaacgc tagttttgca 800
ggaaaggag ccagcgacaa cccttgctcc gaagtgtacc atggacccca 850
cgccaattcg gaagtggagg tgaaatcagt ggtagatttc atccaaaaac 900
atgggaattt caagggttc atcgacctgc acagctactc gcagctgctg 950
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 atctaaattg caggatgggt aaattatccc catctgtcct aatgggctta 2350
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 aggtcctaaa tcaatcatct ggctggata atctcactgc cctggcacat 2450
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 agctgcctct tgtttcattt cacctcagca cgtaccatct gtcccttttgt 2650
 tgttggtgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700
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 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234
 <211> 421
 <212> PRT
 <213> Homo sapiens

<400> 234
 Met Arg Trp Ile Leu Phe Ile Gly Ala Leu Ile Gly Ser Ser Ile
 1 5 10 15
 Cys Gly Gln Glu Lys Phe Phe Gly Asp Gln Val Leu Arg Ile Asn
 20 25 30
 Val Arg Asn Gly Asp Glu Ile Ser Lys Leu Ser Gln Leu Val Asn
 35 40 45
 Ser Asn Asn Leu Lys Leu Asn Phe Trp Lys Ser Pro Ser Ser Phe
 50 55 60
 Asn Arg Pro Val Asp Val Leu Val Pro Ser Val Ser Leu Gln Ala
 65 70 75
 Phe Lys Ser Phe Leu Arg Ser Gln Gly Leu Glu Tyr Ala Val Thr
 80 85 90
 Ile Glu Asp Leu Gln Ala Leu Leu Asp Asn Glu Asp Asp Glu Met
 95 100 105
 Gln His Asn Glu Gly Gln Glu Arg Ser Ser Asn Asn Phe Asn Tyr
 110 115 120
 Gly Ala Tyr His Ser Leu Glu Ala Ile Tyr His Glu Met Asp Asn
 125 130 135
 Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
 140 145 150
 His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
 155 160 165
 Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
 170 175 180
 His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
 185 190 195

Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235

<211> 1743

<212> DNA

<213> Homo sapiens

<400> 235

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tgttccaaaa tggcatctta cctttatgga gtactctttg ctgttggcct 100

ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150
 cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200
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 gagtcagaac atctttctct cccctgtgag tgtctccact tccctggcca 300
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 gtccctctta cttactgtc tccttcaata ggaccttct gatgatgatt 1250
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 cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350
 tgcacaagaa ataacaaacc acatccctct ttctgttctg aggggtgcatt 1400
 tgaccccagt ggagctggat tcgctggcag ggatgccact tccaaggctc 1450
 aatcaccaaa ccatcaacag ggaccccagt cacaagccaa caccattaa 1500

cccagtcag tgcccttttc cacaaattct cccaggtaac tagcttcatg 1550
 ggatgttgct gggttaccat atttccattc cttggggctc ccaggaatgg 1600
 aaatacgcca acccagggtta ggcacctcta ttgcagaatt acaataaacac 1650
 attcaataaa actaaaatat gaattcaaaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
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 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala
 200 205 210

Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe	215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met	230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn	245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe	260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala	275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys	290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser	305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala	320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser	335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser	350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile	365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn	380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile	395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser	410	415	

<210> 237

<211> 23

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 238

ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 239

tgaactggggg tctccaaaac cagc 24

<210> 240

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 240

ggtataggcg gaaggcaaag tcgg 24

<210> 241

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 241

ggcatettac ctttatggag tactctttgc tgttggectc tgtgctcc 48

<210> 242

<211> 2436

<212> DNA

<213> Homo sapiens

<400> 242

ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgcccac gctgagtc aaagattcttc ccaggaacac aaacgtagga 100

gacccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150

ctttctcaag aatcctctgt tctttgcoct ctaaagtctt ggtacatcta 200

ggacccaggg atcttgcttt ccagccacaa agagacagat gaagatgcag 250

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243

<211> 596

<212> PRT

<213> Homo sapiens

<400> 243

Met	Lys	Met	Gln	Lys	Gly	Asn	Val	Leu	Leu	Met	Phe	Gly	Leu	Leu
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Leu	His	Leu	Glu	Ala	Ala	Thr	Asn	Ser	Asn	Glu	Thr	Ser	Thr	Ser
				20					25					30

Ala	Asn	Thr	Gly	Ser	Ser	Val	Ile	Ser	Ser	Gly	Ala	Ser	Thr	Ala
				35					40					45

Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Val	Ser	Thr	Ala
				50					55					60

Thr	Ile	Ser	Gly	Ser	Ser	Val	Thr	Ser	Asn	Gly	Val	Ser	Ile	Val
				65					70					75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala
				80					85					90

Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala
				95					100					105

Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	110	115	120
Thr Asn Ser Glu Ser Ser Thr Pro Ser	Ser Gly Ala Ser Thr Val	125	130	135
Thr Asn Ser Gly Ser Ser Val Thr Ser	Ser Gly Ala Ser Thr Ala	140	145	150
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr Ala	155	160	165
Thr Asn Ser Glu Ser Ser Thr Leu Ser	Ser Gly Ala Ser Thr Ala	170	175	180
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	185	190	195
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	200	205	210
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Arg Ala Ser Thr Ala	215	220	225
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	230	235	240
Thr Asn Ser Glu Ser Arg Thr Thr Ser	Asn Gly Ala Gly Thr Ala	245	250	255
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	260	265	270
Thr Asn Ser Asp Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr Ala	275	280	285
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	290	295	300
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	305	310	315
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Gly Ala Gly Thr Ala	320	325	330
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr Val	335	340	345
Thr Asn Ser Glu Ser Ser Thr Pro Ser	Ser Gly Ala Asn Thr Ala	350	355	360
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr Ala	365	370	375
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ala Ser Thr Ala	380	385	390

Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Val Ser Thr Ala	395	400	405
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Ser Thr Ala	410	415	420
Thr Asn Ser Asp Ser Ser Thr Thr Ser	Ser Glu Ala Ser Thr Ala	425	430	435
Thr Asn Ser Glu Ser Ser Thr Val Ser	Ser Gly Ile Ser Thr Val	440	445	450
Thr Asn Ser Glu Ser Ser Thr Thr Ser	Ser Gly Ala Asn Thr Ala	455	460	465
Thr Asn Ser Gly Ser Ser Val Thr Ser	Ala Gly Ser Gly Thr Ala	470	475	480
Ala Leu Thr Gly Met His Thr Thr Ser	His Ser Ala Ser Thr Ala	485	490	495
Val Ser Glu Ala Lys Pro Gly Gly Ser	Leu Val Pro Trp Glu Ile	500	505	510
Phe Leu Ile Thr Leu Val Ser Val Val	Ala Ala Val Gly Leu Phe	515	520	525
Ala Gly Leu Phe Phe Cys Val Arg Asn	Ser Leu Ser Leu Arg Asn	530	535	540
Thr Phe Asn Thr Ala Val Tyr His Pro	His Gly Leu Asn His Gly	545	550	555
Leu Gly Pro Gly Pro Gly Gly Asn His	Gly Ala Pro His Arg Pro	560	565	570
Arg Trp Ser Pro Asn Trp Phe Trp Arg	Arg Pro Val Ser Ser Ile	575	580	585
Ala Met Glu Met Ser Gly Arg Asn Ser	Gly Pro	590	595	

<210> 244

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 245

gtcagagttg gtggtgtgc tagc 24

<110> 246

<111> 43

<112> DNA

<113> Artificial Sequence

<120>

<123> Synthetic oligonucleotide probe

<400> 246

ggaccagggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<110> 247

<111> 957

<112> DNA

<113> Homo sapiens

<400> 247

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tcctccttc tgctactggg ggccctgtct ggatggggcg ccagcgatga 150
ctccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200
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ctgggaagga agcagagaaa cttggccaag ggtcaacca tgetgctgac 550
caggctggaa aggaagtggg gaagcttggc caaggtgccc accatgctgc 600
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 tacacca 957

<210> 248
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 248
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 20 25 30
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 35 40 45
 Glu Val Gly Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His
 50 55 60
 Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met
 65 70 75
 Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val Gln Gly Leu
 80 85 90
 Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His Gly Ile
 95 100 105
 Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val Asn
 110 115 120
 Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln
 125 130 135
 Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys
 140 145 150
 Leu Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu
 155 160 165
 Val Glu Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala
 170 175 180
 Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser
 185 190 195
 Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser
 200 205 210
 Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly

	215	220	225
Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg			
	230	235	240
Ser Val Ala Asn Ile Met Pro			
	245		

<210> 249
 <211> 23
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 249
 caatatgcat cttgcacgta tgg 23

<210> 250
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 250
 aagctttctt gcttcctttc ctgc 24

<210> 251
 <211> 43
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 251
 tgacccatt gagaaggta ttgaaggat caaccgagg ctg 43

<210> 252
 <211> 3781
 <212> RNA
 <213> Homo sapiens

<400> 252
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 tgacctgac tcaactcagg tccggaggcg ggggcccccg gggcgactcg 150
 gggggggacc gcggggcgga gctgcgcgcc gtgagtcagg ccgagccacc 200
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 ctctgaagaa ttactgttta aaaaaaaaaa a 3761

0100 253
 0110 837
 0120 PFT
 0130 Homo sapiens

0400 253
 Met Leu Arg Thr Ala Met Gly Leu Arg Ser Trp Leu Ala Ala Pro
 1 5 10 15
 Trp Gly Ala Leu Pro Pro Arg Pro Pro Leu Leu Leu Leu Leu Leu
 20 25 30
 Leu Leu Leu Leu Leu Gln Pro Pro Pro Pro Thr Trp Ala Leu Ser
 35 40 45
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu
 50 55 60
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu
 65 70 75
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu
 80 85 90
 Phe Ala Leu Ser Ser Asn Leu Ser Phe Leu Pro Gly Gly Glu Tyr
 95 100 105
 Gln Glu Leu Leu Trp Gly Ala Asp Ala Glu Lys Lys Gln Gln Cys
 110 115 120

Ser Phe Lys Gly Lys Asp Pro Gln Arg Asp Cys Gln Asn Tyr Ile	125	130	135
Lys Ile Leu Leu Pro Leu Ser Gly Ser His Leu Phe Thr Cys Gly	140	145	150
Thr Ala Ala Phe Ser Pro Met Cys Thr Tyr Ile Asn Met Glu Asn	155	160	165
Phe Thr Leu Ala Arg Asp Glu Lys Gly Asn Val Leu Leu Glu Asp	170	175	180
Gly Lys Gly Arg Cys Pro Phe Asp Pro Asn Phe Lys Ser Thr Ala	185	190	195
Leu Val Val Asp Gly Glu Leu Tyr Thr Gly Thr Val Ser Ser Phe	200	205	210
Gln Gly Asn Asp Pro Ala Ile Ser Arg Ser Gln Ser Leu Arg Pro	215	220	225
Thr Lys Thr Glu Ser Ser Leu Asn Trp Leu Gln Asp Pro Ala Phe	230	235	240
Val Ala Ser Ala Tyr Ile Pro Glu Ser Leu Gly Ser Leu Gln Gly	245	250	255
Asp Asp Asp Lys Ile Tyr Phe Phe Phe Ser Glu Thr Gly Gln Glu	260	265	270
Phe Glu Phe Phe Glu Asn Thr Ile Val Ser Arg Ile Ala Arg Ile	275	280	285
Cys Lys Gly Asp Glu Gly Gly Glu Arg Val Leu Gln Gln Arg Trp	290	295	300
Thr Ser Phe Leu Lys Ala Gln Leu Leu Cys Ser Arg Pro Asp Asp	305	310	315
Gly Phe Pro Phe Asn Val Leu Gln Asp Val Phe Thr Leu Ser Pro	320	325	330
Ser Pro Gln Asp Trp Arg Asp Thr Leu Phe Tyr Gly Val Phe Thr	335	340	345
Ser Gln Trp His Arg Gly Thr Thr Glu Gly Ser Ala Val Cys Val	350	355	360
Phe Thr Met Lys Asp Val Gln Arg Val Phe Ser Gly Leu Tyr Lys	365	370	375
Glu Val Asn Arg Glu Thr Gln Gln Trp Tyr Thr Val Thr His Pro	380	385	390
Val Pro Thr Pro Arg Pro Gly Ala Cys Ile Thr Asn Ser Ala Arg	395	400	405

Glu Arg Lys Ile Asn Ser Ser Leu Gln Leu Pro Asp Arg Val Leu	410	415	420
Asn Phe Leu Lys Asp His Phe Leu Met Asp Gly Gln Val Arg Ser	425	430	435
Arg Met Leu Leu Leu Gln Pro Gln Ala Arg Tyr Gln Arg Val Ala	440	445	450
Val His Arg Val Pro Gly Leu His His Thr Tyr Asp Val Leu Phe	455	460	465
Leu Gly Thr Gly Asp Gly Arg Leu His Lys Ala Val Ser Val Gly	470	475	480
Pro Arg Val His Ile Ile Glu Glu Leu Gln Ile Phe Ser Ser Gly	485	490	495
Gln Pro Val Gln Asn Leu Leu Leu Asp Thr His Arg Gly Leu Leu	500	505	510
Tyr Ala Ala Ser His Ser Gly Val Val Gln Val Pro Met Ala Asn	515	520	525
Cys Ser Leu Tyr Arg Ser Cys Gly Asp Cys Leu Leu Ala Arg Asp	530	535	540
Pro Tyr Cys Ala Trp Ser Gly Ser Ser Cys Lys His Val Ser Leu	545	550	555
Tyr Gln Pro Gln Leu Ala Thr Arg Pro Trp Ile Gln Asp Ile Glu	560	565	570
Gly Ala Ser Ala Lys Asp Leu Cys Ser Ala Ser Ser Val Val Ser	575	580	585
Pro Ser Phe Val Pro Thr Gly Glu Lys Pro Cys Glu Gln Val Gln	590	595	600
Phe Gln Pro Asn Thr Val Asn Thr Leu Ala Cys Pro Leu Leu Ser	605	610	615
Asn Leu Ala Thr Arg Leu Trp Leu Arg Asn Gly Ala Pro Val Asn	620	625	630
Ala Ser Ala Ser Cys His Val Leu Pro Thr Gly Asp Leu Leu Leu	635	640	645
Val Gly Thr Gln Gln Leu Gly Glu Phe Gln Cys Trp Ser Leu Glu	650	655	660
Glu Gly Phe Gln Gln Leu Val Ala Ser Tyr Cys Pro Glu Val Val	665	670	675
Glu Asp Gly Val Ala Asp Gln Thr Asp Glu Gly Gly Ser Val Pro	680	685	690

Val Ile Ile Ser Thr Ser Arg Val Ser Ala Pro Ala Gly Gly Lys	705
695	700
Ala Ser Trp Gly Ala Asp Arg Ser Tyr Trp Lys Glu Phe Leu Val	720
710	715
Met Cys Thr Leu Phe Val Leu Ala Val Leu Leu Pro Val Leu Phe	735
725	730
Leu Leu Tyr Arg His Arg Asn Ser Met Lys Val Phe Leu Lys Gln	750
740	745
Gly Glu Cys Ala Ser Val His Pro Lys Thr Cys Pro Val Val Leu	765
755	760
Pro Pro Glu Thr Arg Pro Leu Asn Gly Leu Gly Pro Pro Ser Thr	780
770	775
Pro Leu Asp His Arg Gly Tyr Gln Ser Leu Ser Asp Ser Pro Pro	795
785	790
Gly Ala Arg Val Phe Thr Glu Ser Glu Lys Arg Pro Leu Ser Ile	810
800	805
Gln Asp Ser Phe Val Glu Val Ser Pro Val Cys Pro Arg Pro Arg	825
815	820
Val Arg Leu Gly Ser Glu Ile Arg Asp Ser Val Val	
830	835

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 254

agcccggtgca gaatctgctc ctgg 24

<210> 255

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

tgaagccagg gcagcgtcct ctgg 24

<210> 256

<211> 18

<212> DNA

<213> Artificial Sequence

<200>
<223> Synthetic oligonucleotide probe

<400> 256
gtacaggtg cagttggc 18

<210> 257
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<212> DNA
<213> Artificial Sequence

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agaagccatg tgagcaagtc cagttccagc ccaacacagt g 41

<210> 258
<211> 45
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<210>
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<400> 258
gagctgcaga tcttctcattc gggacagccc gtgcagaatc tgctc 45

<210> 259
<211> 4563
<212> DNA
<213> Homo sapiens

<210>
<221> unsure
<222> 3635
<223> unknown base

<400> 259
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aggcggggac gggagcccg aactgtctgc cgcgcgctc gtgcgcgtcg 150
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 ccagtgaaca atattttct attgtacttt tcgaaccatt ttgtctcatt 4500
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110 - 260

111 - 802

112 - PRT

113 - Homo sapiens

<400> 260

Met	Ala	Ala	Arg	Gly	Arg	Arg	Ala	Trp	Leu	Ser	Val	Leu	Leu	Gly	1	5	10	15
Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	20	25	30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	35	40	45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	50	55	60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	65	70	75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	80	85	90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	95	100	105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	110	115	120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	125	130	135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	140	145	150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	155	160	165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	170	175	180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	185	190	195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	200	205	210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	215	220	225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	230	235	240	
Lys	Cys	Leu	Arg	Glu	Met	Tyr	Thr	Thr	His	Glu	Asp	Val	Glu	Val	245	250	255	
Gly	Arg	Cys	Val	Arg	Arg	Phe	Ala	Gly	Val	Gln	Cys	Val	Trp	Ser	260	265	270	
Tyr	Glu	Met	Arg	Gln	Leu	Phe	Tyr	Glu	Asn	Tyr	Glu	Gln	Asn	Lys				

275										280										285									
Lys Gly Tyr Ile Arg Asp Leu His Asn Ser Lys Ile His Gln Ala	290	295	300																										
Ile Thr Leu His Pro Asn Lys Asn Pro Pro Tyr Gln Tyr Arg Leu	305	310	315																										
His Ser Tyr Met Leu Ser Arg Lys Ile Ser Glu Leu Arg His Arg	320	325	330																										
Thr Ile Gln Leu His Arg Glu Ile Val Leu Met Ser Lys Tyr Ser	335	340	345																										
Asn Thr Glu Ile His Lys Glu Asp Leu Gln Leu Gly Ile Pro Pro	350	355	360																										
Ser Phe Met Arg Phe Gln Pro Arg Gln Arg Glu Glu Ile Leu Glu	365	370	375																										
Trp Glu Phe Leu Thr Gly Lys Tyr Leu Tyr Ser Ala Val Asp Gly	380	385	390																										
Gln Pro Pro Arg Arg Gly Met Asp Ser Ala Gln Arg Glu Ala Leu	395	400	405																										
Asp Asp Ile Val Met Gln Val Met Glu Met Ile Asn Ala Asn Ala	410	415	420																										
Lys Thr Arg Gly Arg Ile Ile Asp Phe Lys Glu Ile Gln Tyr Gly	425	430	435																										
Tyr Arg Arg Val Asn Pro Met Tyr Gly Ala Glu Tyr Ile Leu Asp	440	445	450																										
Leu Leu Leu Leu Tyr Lys Lys His Lys Gly Lys Lys Met Thr Val	455	460	465																										
Pro Val Arg Arg His Ala Tyr Leu Gln Gln Thr Phe Ser Lys Ile	470	475	480																										
Gln Phe Val Glu His Glu Glu Leu Asp Ala Gln Glu Leu Ala Lys	485	490	495																										
Arg Ile Asn Gln Glu Ser Gly Ser Leu Ser Phe Leu Ser Asn Ser	500	505	510																										
Leu Lys Lys Leu Val Pro Phe Gln Leu Pro Gly Ser Lys Ser Glu	515	520	525																										
His Lys Glu Pro Lys Asp Lys Lys Ile Asn Ile Leu Ile Pro Leu	530	535	540																										
Ser Gly Arg Phe Asp Met Phe Val Arg Phe Met Gly Asn Phe Glu	545	550	555																										
Lys Thr Cys Leu Ile Pro Asn Gln Asn Val Lys Leu Val Val Leu																													

560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn Asn	
785	790	795
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800		

<210> 261

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261
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<210> 262
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 262
tcccatttct tccgtggtgc ccag 24

<210> 263
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 263
ccagaagaag tcttcatga tgctcaagta catgcacgac cactac 46

<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

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gttcgggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150
tctttctagt tgcgcttttg ctatggcctt cgtctgtgcg ggcttatccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtag gaagtgttcc ctctggggag ccaggctcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
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tgttttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
gcttcacacc ggaaatagga aagaaaaaac acacggaaaag taccocatc 500
tggtcgatca aaccaaacaa tgtttccatt gttttgcatg cagaggaacc 550
ttatattgaa aatgaagagc cagagccaga gcgggagcca gctgcaaaac 600
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650

ccatatgtta cctcatacaa gtcacctgtc accactttag ataagagcac 700
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 aaactgpgat agaaaaaccc gaagagtttg gaaagcacc cagagagttgg 800
 aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgca 850
 acaggcactt cttagtgcac ccagcaaccc agcatataga gaagatattg 900
 aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950
 gaacataaat taaaaacaat gtataagtcc cagttattgc cagtaggacg 1000
 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
 attctagatc taaactctat gaatatttag atattaaatg tgttccacca 1100
 gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150
 tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga ttttagcaaa 1250
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met	Lys	Pro	Leu	Val	Leu	Leu	Val	Ala	Leu	Leu	Leu	Trp	Pro	Ser
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Ser	Val	Pro	Ala	Tyr	Pro	Ser	Ile	Thr	Val	Thr	Pro	Asp	Glu	Glu
				20					25					30
Gln	Asn	Leu	Asn	His	Tyr	Ile	Gln	Val	Leu	Glu	Asn	Leu	Val	Arg
				35					40					45
Ser	Val	Pro	Ser	Gly	Glu	Pro	Gly	Arg	Glu	Lys	Lys	Ser	Asn	Ser
				50					55					60
Pro	Lys	His	Val	Tyr	Ser	Ile	Ala	Ser	Lys	Gly	Ser	Lys	Phe	Lys
				65					70					75
Glu	Leu	Val	Thr	His	Gly	Asp	Ala	Ser	Thr	Glu	Asn	Asp	Val	Leu
				80					85					90

Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95	100	105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110	115	120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125	130	135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140	145	150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155	160	165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170	175	180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185	190	195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200	205	210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215	220	225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230	235	240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245	250	255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260	265	270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275	280	285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290	295	300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305	310	315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320	325	330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335	340	345
Leu Leu Lys Val Tyr	350		

210 266
 211 2403
 212 DNA

<212> Homo sapiens

<400> 266

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tttjgttctc agtttctacg agctgggtgc aggacagtgg caagtcaactg 200
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 aaa 2403

.110: 267
 .111: 466
 .112: PFT
 .113: Homo sapiens

2400: 267
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 Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala
 20 25 30
 Leu Val Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu

35	40	45
Thr Ser Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe 50 55 60		
His Ala Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser 65 70 75		
Lys Gln Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp 80 85 90		
Ser Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr 95 100 105		
Pro Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile 110 115 120		
Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly 125 130 135		
Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile 140 145 150		
Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala 155 160 165		
Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg 170 175 180		
Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile 185 190 195		
Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu 200 205 210		
Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu 215 220 225		
Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu 230 235 240		
Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile 245 250 255		
Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp 260 265 270		
Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys 275 280 285		
His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys 290 295 300		
Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro 305 310 315		
Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val		

320	325	330
Val Ala Ser Gln Gly Phe Gln Ala Gly	Arg His Tyr Trp Glu Val	
335	340	345
Asp Val Gly Gln Asn Val Gly Trp Tyr	Val Gly Val Cys Arg Asp	
350	355	360
Asp Val Asp Arg Gly Lys Asn Asn Val	Thr Leu Ser Pro Asn Asn	
365	370	375
Gly Tyr Trp Val Leu Arg Leu Thr Thr	Glu His Leu Tyr Phe Thr	
380	385	390
Phe Asn Pro His Phe Ile Ser Leu Pro	Pro Ser Thr Pro Pro Thr	
395	400	405
Arg Val Gly Val Phe Leu Asp Tyr Glu	Gly Gly Thr Ile Ser Phe	
410	415	420
Phe Asn Thr Asn Asp Gln Ser Leu Ile	Tyr Thr Leu Leu Thr Cys	
425	430	435
Gln Phe Glu Gly Leu Leu Arg Pro Tyr	Ile Gln His Ala Met Tyr	
440	445	450
Asp Glu Glu Lys Gly Thr Pro Ile Phe	Ile Cys Pro Val Ser Trp	
455	460	465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
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 aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900

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<210> 269
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 269
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 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala
 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
 95 100 105
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
 110 115 120
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
 155 160 165
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210

Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr	215	220	225
Trp Leu Val Ser Ala Ala His Cys Phe Thr Thr Tyr Lys Asn Pro	230	235	240
Ala Arg Trp Thr Ala Ser Phe Gly Val Thr Ile Lys Pro Ser Lys	245	250	255
Met Lys Arg Gly Leu Arg Arg Ile Ile Val His Glu Lys Tyr Lys	260	265	270
His Pro Ser His Asp Tyr Asp Ile Ser Leu Ala Glu Leu Ser Ser	275	280	285
Pro Val Pro Tyr Thr Asn Ala Val His Arg Val Cys Leu Pro Asp	290	295	300
Ala Ser Tyr Glu Phe Gln Pro Gly Asp Val Met Phe Val Thr Gly	305	310	315
Phe Gly Ala Leu Lys Asn Asp Gly Tyr Ser Gln Asn His Leu Arg	320	325	330
Gln Ala Gln Val Thr Leu Ile Asp Ala Thr Thr Cys Asn Glu Pro	335	340	345
Gln Ala Tyr Asn Asp Ala Ile Thr Pro Arg Met Leu Cys Ala Gly	350	355	360
Ser Leu Glu Gly Lys Thr Asp Ala Cys Gln Gly Asp Ser Gly Gly	365	370	375
Pro Leu Val Ser Ser Asp Ala Arg Asp Ile Trp Tyr Leu Ala Gly	380	385	390
Ile Val Ser Trp Gly Asp Glu Cys Ala Lys Pro Asn Lys Pro Gly	395	400	405
Val Tyr Thr Arg Val Thr Ala Leu Arg Asp Trp Ile Thr Ser Lys	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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catgctgggc tctccctgcc ttctgtggct cctggcctg acctctcttg 200
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<210> 271

<211> 238

<212> FRT

<213> Homo sapiens

<400> 271

Met	Leu	Gly	Ser	Pro	Cys	Leu	Leu	Trp	Leu	Leu	Ala	Val	Thr	Phe
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Leu	Val	Pro	Arg	Ala	Gln	Pro	Leu	Ala	Pro	Gln	Asp	Phe	Glu	Glu
			20					25						30
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40						45

Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys	50	55	60
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly	65	70	75
Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	80	85	90
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	95	100	105
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	110	115	120
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	125	130	135
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	140	145	150
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	155	160	165
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	170	175	180
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	185	190	195
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	200	205	210
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	215	220	225
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			230	235	

<210> 272
 <211> 2397
 <212> DNA
 <213> Homo sapiens

<400> 272
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 cccaggcggg cgtggggcac cgggccccagc gccgacgac gctgccgttt 150
 tgccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200
 gtcacaaatg gccagagaag attccgtgaa gtgtctgcgc tgccctgctct 250
 accccctcaa tctgctcttt tggttaatgt ccatcagtgt gttggcagtt 300

tctgcttgga tgagggacta cctaaataat gttctcactt taactgcaga 350
aaagagggtg gaggaagcag tcattttgac ttactttcct gtggttcac 400
cggtcacgat tgggttttgc tgtttcotta tcattgtggg gatgttagga 450
tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500
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aaagccagga tgacaaatta tggattacct agatatacgt ggcttactca 650
tgcttggaat ttttttcaga gagagtttaa gtgctgtgga gtagtatatt 700
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tgtgttagag aattcccagg atgttccaaa caggccccc aggaagatct 800
cagtgaactt tatcaagagg gttgtgggaa gaaaatgtat tcctttttga 850
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cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250
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<210> 273

<211> 305

<212> PFT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120

Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser	170	175	180
Cys	Cys	Val	Arg	Glu	Phe	Pro	Gly	Cys	Ser	Lys	Gln	Ala	His	Gln	185	190	195
Glu	Asp	Leu	Ser	Asp	Leu	Tyr	Gln	Glu	Gly	Cys	Gly	Lys	Lys	Met	200	205	210
Tyr	Ser	Phe	Leu	Arg	Gly	Thr	Lys	Gln	Leu	Gln	Val	Leu	Arg	Phe	215	220	225
Leu	Gly	Ile	Ser	Ile	Gly	Val	Thr	Gln	Ile	Leu	Ala	Met	Ile	Leu	230	235	240
Thr	Ile	Thr	Leu	Leu	Trp	Ala	Leu	Tyr	Tyr	Asp	Arg	Arg	Glu	Pro	245	250	255
Gly	Thr	Asp	Gln	Met	Met	Ser	Leu	Lys	Asn	Asp	Asn	Ser	Gln	His	260	265	270
Leu	Ser	Cys	Pro	Ser	Val	Glu	Leu	Leu	Lys	Pro	Ser	Leu	Ser	Arg	275	280	285
Ile	Phe	Glu	His	Thr	Ser	Met	Ala	Asn	Ser	Phe	Asn	Thr	His	Phe	290	295	300
Glu	Met	Glu	Glu	Leu											305		

<210> 274

<211> 2063

<212> DNA

<213> Homo sapiens

<400> 274

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agagccagca tgttacagga tctgacagt gacaaacctc tgaacagcct 250

cgatgtcaaa cccctgcgca aaccccgat cccatggag accttcagaa 300

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 caaaaaaaaaaaa aaa 2063

<210> 275
 <211> 432
 <212> PRT
 <213> Homo sapiens

<400> 275
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 Lys Val Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser
 35 40 45
 Ile Ile Ile Val Val Val Leu Ile Lys Val Ile Leu Asp Lys Tyr
 50 55 60
 Tyr Phe Leu Cys Gly Gln Pro Leu His Phe Ile Pro Arg Lys Gln
 65 70 75
 Leu Cys Asp Gly Glu Leu Asp Cys Pro Leu Gly Glu Asp Glu Glu
 80 85 90
 His Cys Val Lys Ser Phe Pro Glu Gly Pro Ala Val Ala Val Arg
 95 100 105
 Leu Ser Lys Asp Arg Ser Thr Leu Gln Val Leu Asp Ser Ala Thr
 110 115 120
 Gly Asn Trp Phe Ser Ala Cys Phe Asp Asn Phe Thr Glu Ala Leu
 125 130 135
 Ala Glu Thr Ala Cys Arg Gln Met Gly Tyr Ser Arg Ala Val Glu
 140 145 150
 Ile Gly Pro Asp Gln Asp Leu Asp Val Val Glu Ile Thr Glu Asn
 155 160 165
 Ser Gln Glu Leu Arg Met Arg Asn Ser Ser Gly Pro Cys Leu Ser
 170 175 180

Gly Ser Leu Val Ser Leu His Cys Leu Ala Cys Gly Lys Ser Leu	185	190	195
Lys Thr Pro Arg Val Val Gly Gly Glu Glu Ala Ser Val Asp Ser	200	205	210
Trp Pro Trp Gln Val Ser Ile Gln Tyr Asp Lys Gln His Val Cys	215	220	225
Gly Gly Ser Ile Leu Asp Pro His Trp Val Leu Thr Ala Ala His	230	235	240
Cys Phe Arg Lys His Thr Asp Val Phe Asn Trp Lys Val Arg Ala	245	250	255
Gly Ser Asp Lys Leu Gly Ser Phe Pro Ser Leu Ala Val Ala Lys	260	265	270
Ile Ile Ile Ile Glu Phe Asn Pro Met Tyr Pro Lys Asp Asn Asp	275	280	285
Ile Ala Leu Met Lys Leu Gln Phe Pro Leu Thr Phe Ser Gly Thr	290	295	300
Val Arg Pro Ile Cys Leu Pro Phe Phe Asp Glu Glu Leu Thr Pro	305	310	315
Ala Thr Pro Leu Trp Ile Ile Gly Trp Gly Phe Thr Lys Gln Asn	320	325	330
Gly Gly Lys Met Ser Asp Ile Leu Leu Gln Ala Ser Val Gln Val	335	340	345
Ile Asp Ser Thr Arg Cys Asn Ala Asp Asp Ala Tyr Gln Gly Glu	350	355	360
Val Thr Glu Lys Met Met Cys Ala Gly Ile Pro Glu Gly Gly Val	365	370	375
Asp Thr Cys Gln Gly Asp Ser Gly Gly Pro Leu Met Tyr Gln Ser	380	385	390
Asp Gln Trp His Val Val Gly Ile Val Ser Trp Gly Tyr Gly Cys	395	400	405
Gly Gly Pro Ser Thr Pro Gly Val Tyr Thr Lys Val Ser Ala Tyr	410	415	420
Leu Asn Trp Ile Tyr Asn Val Trp Lys Ala Glu Leu	425	430	

4210 276
 4211 3143
 4212 DNA
 4213 Homo sapiens

<400> 276

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 ctgagaggag cttctgctac tctgcctcac tgatgacact cagcagggtg 2550
 atgcacagca gtctgcctcc cctatgggac tccctctac caagcacatg 2600
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 cagaaacaca gtytttcaag agacctaaa aaactgcct gtcccaggac 2750
 cctatggtaa tgaacaccaa acatctaaac aatcatatgc taacatgcca 2800
 ctctggaaa ctccactctg aagctgcgc tttggacacc aacactcct 2850

tctccagggt tcatgcagggt atctgctccc tctgtctcc cttaccagtc 2900
 gtgcaccggt gactcccagg aagtctttcc tgaagtctga ccacctttct 2950
 tcttgcttca gttggggtag actctgates cttctgacct ggcagaatgg 3000
 caggggtaat ctgagccttc ttcaactcctt taccctagct gacccttca 3050
 cctctccccc tcccttttcc tttgttttgg gattcagaaa actgcttgtc 3100
 agagaactgtt tattttttat taaaaatata aggccttaaaa aaa 3143

<210> 277
 <211> 761
 <212> PFT
 <213> Homo sapiens

<400> 277
 Met Ala Leu Pro Ala Leu Gly Leu Asp Pro Trp Ser Leu Leu Gly
 1 5 10 15
 Leu Phe Leu Phe Gln Leu Leu Gln Leu Leu Leu Pro Thr Thr Thr
 20 25 30
 Ala Gly Gly Gly Gly Gln Gly Pro Met Pro Arg Val Arg Tyr Tyr
 35 40 45
 Ala Gly Asp Glu Arg Arg Ala Leu Ser Phe Phe His Gln Lys Gly
 50 55 60
 Leu Gln Asp Phe Asp Thr Leu Leu Leu Ser Gly Asp Gly Asn Thr
 65 70 75
 Leu Tyr Val Gly Ala Arg Glu Ala Ile Leu Ala Leu Asp Ile Gln
 80 85 90
 Asp Pro Gly Val Pro Arg Leu Lys Asn Met Ile Pro Trp Pro Ala
 95 100 105
 Ser Asp Arg Lys Lys Ser Glu Cys Ala Phe Lys Lys Lys Ser Asn
 110 115 120
 Glu Thr Gln Cys Phe Asn Phe Ile Arg Val Leu Val Ser Tyr Asn
 125 130 135
 Val Thr His Leu Tyr Thr Cys Gly Thr Phe Ala Phe Ser Pro Ala
 140 145 150
 Cys Thr Phe Ile Glu Leu Gln Asp Ser Tyr Leu Leu Pro Ile Ser
 155 160 165
 Glu Asp Lys Val Met Glu Gly Lys Gly Gln Ser Pro Phe Asp Pro
 170 175 180
 Ala His Lys His Thr Ala Val Leu Val Asp Gly Met Leu Tyr Ser
 185 190 195

Gly Thr Met Asn Asn Phe Leu Gly Ser Glu Pro Ile Leu Met Arg	200	205	210
Thr Leu Gly Ser Gln Pro Val Leu Lys Thr Asp Asn Phe Leu Arg	215	220	225
Trp Leu His His Asp Ala Ser Phe Val Ala Ala Ile Pro Ser Thr	230	235	240
Gln Val Val Tyr Phe Phe Phe Glu Glu Thr Ala Ser Glu Phe Asp	245	250	255
Phe Phe Glu Arg Leu His Thr Ser Arg Val Ala Arg Val Cys Lys	260	265	270
Asn Asp Val Gly Gly Glu Lys Leu Leu Gln Lys Lys Trp Thr Thr	275	280	285
Phe Leu Lys Ala Gln Leu Leu Cys Thr Gln Pro Gly Gln Leu Pro	290	295	300
Phe Asn Val Ile Arg His Ala Val Leu Leu Pro Ala Asp Ser Pro	305	310	315
Thr Ala Pro His Ile Tyr Ala Val Phe Thr Ser Gln Trp Gln Val	320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys Ala Phe Ser Leu Leu Asp	335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr Lys Glu Leu Asn Lys Glu	350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly Pro Glu Thr Asn Pro Arg	365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser Ser Asp Lys Ala Leu Thr	380	385	390
Phe Met Lys Asp His Phe Leu Met Asp Glu Gln Val Val Gly Thr	395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu Tyr Thr Arg Leu Ala Val	410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His Ser His Leu Val Met Tyr	425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His Lys Ala Val Val Ser Gly	440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu Ile Gln Leu Phe Pro Asp	455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu Ala Pro Thr Gln Gly Ala	470	475	480

Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	575	580	585
Leu Ala Ser Tyr Tyr Trp Ser His Gly	Pro Ala Ala Val Pro Glu	590	595	600
Ala Ser Ser Thr Val Tyr Asn Gly Ser	Leu Leu Leu Ile Val Gln	605	610	615
Asp Gly Val Gly Gly Leu Tyr Gln Cys	Trp Ala Thr Glu Asn Gly	620	625	630
Phe Ser Tyr Pro Val Ile Ser Tyr Trp	Val Asp Ser Gln Asp Gln	635	640	645
Thr Leu Ala Leu Asp Pro Glu Leu Ala	Gly Ile Pro Arg Glu His	650	655	660
Val Lys Val Pro Leu Thr Arg Val Ser	Gly Gly Ala Ala Leu Ala	665	670	675
Ala Gln Gln Ser Tyr Trp Pro His Phe	Val Thr Val Thr Val Leu	680	685	690
Phe Ala Leu Val Leu Ser Gly Ala Leu	Ile Ile Leu Val Ala Ser	695	700	705
Pro Leu Arg Ala Leu Arg Ala Arg Gly	Lys Val Gln Gly Cys Glu	710	715	720
Thr Leu Arg Pro Gly Glu Lys Ala Pro	Leu Ser Arg Glu Gln His	725	730	735
Leu Gln Ser Pro Lys Glu Cys Arg Thr	Ser Ala Ser Asp Val Asp	740	745	750
Ala Asp Asn Asn Cys Leu Gly Thr Glu	Val Ala	755	760	

<210> 278
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 278
ctgtgtgtga aatctggcgt ggag 24

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 279
gtctggtcct ggtgtccac ccag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
catcttgta tgcacctggg aaccaccaca ggtcgtctcc acaag 45

<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

<400> 281
agggtccctt agccgggggc agggcgcgca gccaggctg agatccgcgg 50
cttcogtaga agtgagcatg gctgggcagc gagtgttct tctagtggc 100
ttccttctcc ctggggctct gctctcagag gctgccaaaa tctgacaat 150
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200
ttcttcaaga tcacgggtcat aatgtcacca tgcttaacca caaaagaggt 250
ctttttatgc cagattttta aaaggaagaa aaatcatatc aagttatcag 300
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450

ggatatcatg gattccttaa agaatgagaa cttegacatg gtgatagttg 500
 aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550
 tttgtggcca ttctttccac ttcattegge tctttggaat ttgggctacc 600
 aatcccttg tcttatgttc cagtattccg ttcttgctg actgatcaca 650
 tggacttctg gggccgagtg aagaatttcc tgatgttctt tagtttctgc 700
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 agtaccacaa gacttgaga acttcattgc caagtttggg gactctgggt 950
 ttgtccttgt gacctgggc tccatggtga acacctgtca gaatccggaa 1000
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 atgtgaaaat tgtggactgg ctctctcaga gtgacctctt ggctcaccac 1150
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 ctgaaaacat ggtccgagta gaagccaaa agtttggtgt ttctattcag 1300
 ttaaagaagc tcaaggcaga gacattggct ctttaagatga aacaaatcat 1350
 ggaagacaag agatacaagt ccgcggcagt ggctgcaggt gtcacctgc 1400
 gctcccacc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450
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 gccctggcat gacagtagc ttttgcgtt ctgctggggc 1550
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 tgggtggctgc gtggggccag aaaggtgaag gagacataag gccaggtgca 1650
 gccttggcgg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700
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 tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800
 attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850

ttccagtcct cttgtccctcc tttgtttgcc atcagcaagg gctatgctgt 1900
gattctgtct ctgagtgaact tggaccactg acctcagat ttccagcctt 1950
aaaatccacc ttcccttctca tggcctctc cgaatcacac cctgactctt 2000
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gtccctgtct ctggtgccc aagtgcgtc cttcttggt gagcaggcat 2250
ggagactgta ggtttccaga tttcctgaaa aataaaagtt tacagcgtta 2300
ttcttcccca acctcactaa 2320

<010> 282
<011> 523
<012> PRT
<013> Homo sapiens

<000> 282
Met Ala Gly Gln Arg Val Leu Leu Leu Val Gly Phe Leu Leu Pro
1 5 10 15
Gly Val Leu Leu Ser Glu Ala Ala Lys Ile Leu Thr Ile Ser Thr
20 25 30
Val Gly Gly Ser His Tyr Leu Leu Met Asp Arg Val Ser Gln Ile
35 40 45
Leu Gln Asp His Gly His Asn Val Thr Met Leu Asn His Lys Arg
50 55 60
Gly Pro Phe Met Pro Asp Phe Lys Lys Glu Glu Lys Ser Tyr Gln
65 70 75
Val Ile Ser Trp Leu Ala Pro Glu Asp His Gln Arg Glu Phe Lys
80 85 90
Lys Ser Phe Asp Phe Phe Leu Glu Glu Thr Leu Gly Gly Arg Gly
95 100 105
Lys Phe Glu Asn Leu Leu Asn Val Leu Glu Tyr Leu Ala Leu Gln
110 115 120
Cys Ser His Phe Leu Asn Arg Lys Asp Ile Met Asp Ser Leu Lys
125 130 135
Asn Glu Asn Phe Asp Met Val Ile Val Glu Thr Phe Asp Tyr Cys
140 145 150
Pro Phe Leu Ile Ala Glu Lys Leu Gly Lys Pro Phe Val Ala Ile

155	160	165
Leu Ser Thr Ser Phe Gly Ser Leu Glu	Phe Gly Leu Pro Ile Pro	
170	175	180
Leu Ser Tyr Val Pro Val Phe Arg Ser	Leu Leu Thr Asp His Met	
185	190	195
Asp Phe Trp Gly Arg Val Lys Asn Phe	Leu Met Phe Phe Ser Phe	
200	205	210
Cys Arg Arg Gln Gln His Met Gln Ser	Thr Phe Asp Asn Thr Ile	
215	220	225
Lys Glu His Phe Thr Glu Gly Ser Arg	Pro Val Leu Ser His Leu	
230	235	240
Leu Leu Lys Ala Glu Leu Trp Phe Ile	Asn Ser Asp Phe Ala Phe	
245	250	255
Asp Phe Ala Arg Pro Leu Leu Pro Asn	Thr Val Tyr Val Gly Gly	
260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	

	440		445		450
Pro Thr Gln Arg	Leu Val Gly Trp Ile Asp His Val Leu Gln Thr				
	455		460		465
Gly Gly Ala Thr	His Leu Lys Pro Tyr Val Phe Gln Gln Pro Trp				
	470		475		480
His Glu Gln Tyr	Leu Phe Asp Val Phe Val Phe Leu Leu Gly Leu				
	485		490		495
Thr Leu Gly Thr	Leu Trp Leu Cys Gly Lys Leu Leu Gly Met Ala				
	500		505		510
Val Trp Trp Leu	Arg Gly Ala Arg Lys Val Lys Glu Thr				
	515		520		

<210> 283

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 283

tgacttttgcg cacctacccc aag; 24

<210> 284

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 284

ctaggttggt ctccaaagag aggg 24

<210> 285

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 285

cccaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 286

gggctgtga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50

ggttgagggg ctgoototgg catatgcaca cactacacaa ttctgtcaca 100
 ccogtcacac aacataacca tgtttotocat ccccccaggt ccagccctca 150
 gtgctgtccc atncagcagg gctacootga agctotgggt gcagccctcc 200
 cgtccagtgg gcaggcggtt tcatccctcc tttctctccc aaagcccaac 250
 tgctgtcact gcctgtcttg ccaaggagga gggaaactgca gtgacagcag 300
 gagtaagagt gggagggcagg acagagctgg gacacaggta tggagagggg 350
 gttcagcgag cctagagagg gcagactatc aggggtgcgg cggtgagaat 400
 ccaggagagag gajcgghaac agaagagggg cagaagacgg gggcacttgt 450
 gggttgcaga gccctcagc catgttggga gccaaagcac actggctacc 500
 aggtccctca cacagtcccg ggtgccttt gttctgggtg cttctggccc 550
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 gggagcagcc ctgggagagg caccctctgg gcgagtggca tttgctggg 700
 tccgaajcca ccaccatgag ccagcagggg aaaccggcaa tggcaccagt 750
 ggggccatct acttcagaca ggtccctggg aaacagggcg gtggctttga 800
 ccgggcctct ggtccctctg tagccctgt ccggggtgtc tacagcttcc 850
 ggttccatgt ggtjaaggtg tacaacccgc aaactgtcca ggtgagcctg 900
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 gaccggggag gcagccacca gctctgtgt actgccttg gacctgggg 1000
 accgagtgtc tctggcctg cgtcggggga atctactgg tggttggaaa 1050
 tactcaagtt tctctgggtt cctcatcttc cctctctgag gacccaagtc 1100
 tttcaagcac aagaatccag cccctgacaa ctttctcttg cctctcttg 1150
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 cctctttgca tgggacctg tgcacaaac ccaagtttaa gagaagagta 1250
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 ctcggttcc cccacccag cttctgtctc aatgctgac agggacaggt 1450

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 ccacctcctg aaactgctcc acctttgaag tttgaaactt agtccctcca 1950
 cactctgaact gctgcctcct tctcccagc tctctcactg agttatcttc 2000
 actgtacctg ttccagcata tcccactat ctctctttct cctgactctg 2050
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 cttccttca gacctctcc tgcagtatg ctaaaacctc cctctctctt 2150
 tcttatcccg ctgtccatt ggcccagcct ggatgaatct atcaataaaa 2200
 caactagaga atgggtggta gtgagacact atagaattac taaggagaag 2250
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 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287

<211> 295

<212> PRT

<213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
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Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75

Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn		
	80	90
Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu		
	95	105
Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val		
	110	120
Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn		
	125	135
Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val		
	140	150
Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala		
	155	165
Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser		
	170	180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser		
	185	195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu		
	200	205

<210> 288
 <211> 24
 <212> RNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 288
 aggcagccac cagctctgtg ctac 24

<210> 289
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 289
 ccagagaggga agatgaggaa gccagag 27

<210> 290
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 290
ctgtgtact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291
<211> 1570
<212> DNA
<213> Homo sapiens

<400> 291
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ccctggcccc gggggccggg gcatgggcca ggggcgcgg gtgaagcggc 150
ttcccgcggg gccgtgactg ggccggcttc agccatgaag accctcatag 200
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atggggcact ggtaccagca tctctccgc cctccaggac ctcttctctg 350
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agagcccac accatcccca agctggagca cccaaccag caagacatcg 1250
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 tttgctctgt aaatttggaa gtgtcatggg tgtctgtggg ttatttaaaa 1450
 gaaattataa caattttgct aaacccaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1550
 aaaaaaaaaa aaaaaaaaaa 1570

<210> 292
 <211> 388
 <212> FET
 <213> Homo sapiens

<400> 292
 Met Lys Thr Leu Ile Ala Ala Tyr Ser Gly Val Leu Arg Gly Glu
 1 5 10 15
 Arg Gln Ala Glu Ala Asp Arg Ser Gln Arg Ser His Gly Gly Pro
 20 25 30
 Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser
 35 40 45
 Ile Leu Ser Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn
 50 55 60
 Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln
 65 70 75
 Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Ala Ile
 80 85 90
 Leu Met Tyr Ile Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
 95 100 105
 Tyr Phe Thr Trp Leu Val Phe Asp Trp Asn Thr Pro Lys Lys Gly
 110 115 120
 Gly Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr
 125 130 135
 Phe Arg Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu
 140 145 150
 Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile
 155 160 165
 Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu
 170 175 180

Val Ser Lys Lys Phe Pro Gly Ile Arg	Pro Tyr Leu Ala Thr Leu	185	190	195
Ala Gly Asn Phe Arg Met Pro Val Leu	Arg Glu Tyr Leu Met Ser	200	205	210
Gly Gly Ile Cys Pro Val Ser Arg Asp	Thr Ile Asp Tyr Leu Leu	215	220	225
Ser Lys Asn Gly Ser Gly Asn Ala Ile	Ile Ile Val Val Gly Gly	230	235	240
Ala Ala Glu Ser Leu Ser Ser Met Pro	Gly Lys Asn Ala Val Thr	245	250	255
Leu Arg Asn Arg Lys Gly Phe Val Lys	Leu Ala Leu Arg His Gly	260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe	Gly Glu Asn Glu Val Tyr	275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser	Trp Gly Arg Trp Val Gln	290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe	Ala Pro Cys Ile Phe His	305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr	Trp Gly Leu Val Pro Tyr	320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly	Glu Pro Ile Thr Ile Pro	335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp	Ile Asp Leu Tyr His Thr	350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu	Phe Asp Lys His Lys Thr	365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val	Leu Glu Val Asn	380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 223

gcttacctgg ttcccatata ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 244

ccacacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial Sequence

<270>

<213> Synthetic oligonucleotide probe

<400> 295

acgcatgaat tgtacaaagc aggtgatctt cgaggagggc tctggggcc 50

<210> 296

<211> 3060

<212> DNA

<213> Homo sapiens

<400> 296

gggggggggg atggggggcg gggggggggg gcgcgcact cgctgaggcc 50
ccgacgcagg gcggggcggg gcccgaggcc gaggagcgcg gcggccagag 100
ggggggcgcg gaggcgagcg cggggagccc cggcgagcga gcaggtggcg 150
ggggggcgag gcttggtccg ccgggaagccc tgagggcagc tgttccact 200
gggtctgctg accttggtgc ttggacggt gtctcagcg aggggcctg 250
caccgctcc tgagcagcg catgggctg ctggccttc tgaagacca 300
cttctgctg cactgctgg tcggtttgt ctctggtg agtggtctg 350
tcctcaact cgtccagctg tgcagctg cgtctggcc ggtcagcaag 400
cagctctacc gccgctcaa ctgcgcctc gctactcac tctggagcca 450
actggtcatg ctgctggagt ggtggtctg caccgagtgt acactgttca 500
cgaaccaggc caccgtagag ccttttggga aggagcagc agtcacatc 550
cgaaccaca acttcagat cgaactctc tgtgggtgga ccattgtgtga 600
gggcttcgga gtgctgggga gctccaagg ctctgctaag aaggagctgc 650
tctagtgcc cctcatcgcc tggacgtggt actttctgga gattgtgttc 700
tccaagggga agtgggagga ggaacgggac acgtggctg aagggtgag 750
ggcctgtcg gactaccgc agtacatgtg gttctctctg tactgcgagg 800

ggaagcgctt caaggagacc aagcaccggg ttagcatgga ggtggcggt 850
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 cttcaccacc gaagtcaagt gctccgggg gacagtcca gctgtctatg 950
 atgtaacct gaacttcaga ggaaacaaga accgtacct gctggggatc 1000
 ctctacggga agaagtaaga ggcggacatg tgggtgagga gatttcctct 1050
 ggaagacatc ccgtggatg aaaaggaagc agctcagtgg cttcataaac 1100
 tgtaccagga gaaggacgg ctccaggaga tatataatca gaagggcatg 1150
 tttccagggg agcagtttaa gctgcccgg aggcctgga cctcctgaa 1200
 cttctgtcc tgggccacca ttctctgtc tccctcttc agttttgtct 1250
 tgggctctt tgcagcgga tcacctctc tgatctgac tttcttgggg 1300
 tttgtggag cagcttctt tggagttcg agactgatag gagaatcgt 1350
 tgaacctgg aggtggagat tgcagtgagc tgagatggca tcaactgtact 1400
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 aaaaaccca gaaattctgg agttgaactg tctagttact gacatgaaa 1500
 attcaactaga ggtgaacag cagatttgag caggcaaaa aaaatcagca 1550
 agcttgaaga tggtaacctg agattttca ggtaatgaa aaaagaatga 1600
 agaaaaatta acagctcag agaccatgg tgcacctca cacaatatca 1650
 catatgatg atgaggtcc cagaaggaga ggagagaaag ggtcagaaag 1700
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 cagaaatcat gggagccagg agatagtgg atgaacactg ttgaaggcaa 1950
 aacctcaac tgtaattatt ggactttga gtcttagatg gtctgaact 2000
 ctttgtcttc agggacagtt ttcaattta atccctaata acaattagtc 2050
 aagcttctt gactgtagg aaggctgtc tttagccgg gcacagtggc 2100
 ttacacctgt aatccagca ctttgggagg ccagagggg tggatcattt 2150
 ggggtcaggc tgatctcaaa ctctgagtt caggtgatct gcccgctca 2200
 gctcccaaa gtgttgtgat tgcaggcgtg agcactggc cctggccgga 2250

atttcttttt aaggetgaat gatgggggca aggcacgatg gctcacgctt 1300
 gtgatcccaa gtagcttgga ttgtaaacat gcaccaccat gcttggttaa 1350
 tttttgtatt tttagtagag acgtgttagc caggttggtc togatctctt 1400
 gacctcaagt gaccacctgc ctcagcctcc caaagtaactg ggattacagg 1450
 cgtgagccac tgtgcttggc cttgagcacc ttgtgatgtg cttattggcc 1500
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 1550
 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 1600
 ttgttctgtt gccacggctg gactacagtg gcacagtctt ggctcactgc 1650
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 ttgtggagac agcatttcac catgatgccc aggttggtct tgaactcctg 1800
 agctcaagtg atctgcctgc ttcagcctcc caaagtactg ggattacaga 1850
 catgagccac tgcacctggc aaactcccaa aattcaacac acacacaaa 1900
 aaaaccacct gattcaaaat gggcagaggg gccgggtgtg gcccacaacta 1950
 ccaggagagac tgaagtggga ggatcgcttg ggcattgagaa gtcgaggctg 3000
 cagtgagtcg aggttggtgc actgcattcc agcctggaca acagagttag 3050
 accctgtctc 3060

<210> 297
 <211> 368
 <212> PRT
 <213> Homo sapiens

<400> 297
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu
 1 5 10 15
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe
 20 25 30
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu
 35 40 45
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln
 50 55 60
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu
 65 70 75
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala

80	85	90
Val Ile Ile Leu Asn His Asn Phe Glu	Ile Asp Phe Leu Cys Gly	
95	100	105
Trp Thr Met Cys Glu Arg Phe Gly Val	Leu Gly Ser Ser Lys Val	
110	115	120
Leu Ala Lys Lys Glu Leu Leu Tyr Val	Pro Leu Ile Gly Trp Thr	
125	130	135
Trp Tyr Phe Leu Glu Ile Val Phe Cys	Lys Arg Lys Trp Glu Glu	
140	145	150
Asp Arg Asp Thr Val Val Glu Gly Leu	Arg Arg Leu Ser Asp Tyr	
155	160	165
Pro Glu Tyr Met Trp Phe Leu Leu Tyr	Cys Glu Gly Thr Arg Phe	
170	175	180
Thr Glu Thr Lys His Arg Val Ser Met	Glu Val Ala Ala Ala Lys	
185	190	195
Gly Leu Pro Val Leu Lys Tyr His Leu	Leu Pro Arg Thr Lys Gly	
200	205	210
Phe Thr Thr Ala Val Lys Cys Leu Arg	Gly Thr Val Ala Ala Val	
215	220	225
Tyr Asp Val Thr Leu Asn Phe Arg Gly	Asn Lys Asn Pro Ser Leu	
230	235	240
Leu Gly Ile Leu Tyr Gly Lys Lys Tyr	Glu Ala Asp Met Cys Val	
245	250	255
Arg Arg Phe Pro Leu Glu Asp Ile Pro	Leu Asp Glu Lys Glu Ala	
260	265	270
Ala Gln Trp Leu His Lys Leu Tyr Gln	Glu Lys Asp Ala Leu Gln	
275	280	285
Glu Ile Tyr Asn Gln Lys Gly Met Phe	Pro Gly Glu Gln Phe Lys	
290	295	300
Pro Ala Arg Arg Pro Trp Thr Leu Leu	Asn Phe Leu Ser Trp Ala	
305	310	315
Thr Ile Leu Leu Ser Pro Leu Phe Ser	Phe Val Leu Gly Val Phe	
320	325	330
Ala Ser Gly Ser Pro Leu Leu Ile Leu	Thr Phe Leu Gly Phe Val	
335	340	345
Gly Ala Ala Ser Phe Gly Val Arg Arg	Leu Ile Gly Glu Ser Leu	
350	355	360
Glu Pro Gly Arg Trp Arg Leu Gln		

<210> 298
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 298
 cttctctgtt ggtggacca tgtg 24

<210> 299
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 299
 ggtacctcca tgctaacgag g 21

<210> 300
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 300
 ccaagttcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301
 <211> 1334
 <212> DNA
 <213> Homo sapiens

<400> 301
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 tgtctctggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100
 tgcctttagca ctggggcact tcttgcttat ttcttttgta ggaaaggggc 150
 tcagtttgct ttgtgggggt ggtggcagga aggccggctt acgcctgata 200
 cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250
 tagctggggg ctgagacctg cttctcagt aaaattcctg ggatctgctt 300
 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350
 ttctctctgt tcttaggata aaagtattta gagctacaag agccctcatg 400

gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgtttctct 450
 tgtcgttctt gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600
 ctggcctgac agaattctat cttgtttaat gctctcataa gaccacttgt 650
 ttcccttttg cagcaactgc cactcagttg tatctttatg tgcgtttgtg 700
 gttgtatggg ttgtgtctgt tcccagaat gccagctct gagctgcgtg 750
 agggccaagg gcattgctgt gctgcccagg tatagtgctt acatgtgggtg 800
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850
 aaatctctca gttcaccaga tgggtgtaggg cccagcattg taaattcaca 900
 cgttgactgt gcttgtgaat tatctgggga tgcaggtctt gattcagtag 950
 gccaggttg ggcattctta aaaaactccc acgtgatgct gatgctggtc 1000
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050
 tggctcacac ctatgatccc agcactttgg gaggtgagg caggctgac 1100
 acctggagtc aggatctcaa gactagcttg gccacatgg tggaacccca 1150
 tctgtactaa aaatacacia attagctggg catggtggca catgctgtta 1200
 gtcccagcta cttggggagg tgaagcaaga gaatcgcttg aacctgggag 1250
 ggggaggttg cagtgagccg agatcaggcc actgtattcc aaccaggggtg 1300
 ccagagttag actctatgtc caaaaaaaaa aaaa 1334

<210> 302

<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

Met	His	His	Ser	Leu	Gln	Cys	Pro	Gly	Ala	Ala	Thr	Arg	His	Ile
1				5				10						15

His	Leu	Cys	Val	Cys	Phe	Ser	Phe	Ala	Leu	Ala	Leu	Gly	His	Phe
			20					25						30

Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
			35					40						45

Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
			50				55							60

Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	65	70	75
Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr			
	80	85	90
Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln			
	95	100	105
Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu			
	110	115	120
Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr			
	125	130	135
Cys Gly Val Leu Leu Ser Phe Leu			
	140		

<210> 303
 <211> 1768
 <212> DNA
 <213> Homo sapiens

<400> 303
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 aaggtgctgt gattataggt gtaagccacc gtgtctggcc totgaacaac 100
 ttttccagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150
 tatgtctgtg tggctagtgc tectactcct acctacatta aaatctgttt 200
 tttgtttctt tgtaactaga ctttaccttc ctaacacaga ggatctgtca 250
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300
 ttctaccac accgtccctt cgaagccggg gacagctca ccttgcctggc 350
 ctctcgttgg agcagtgcct tcaccaactg tctcagctct ggaggcactg 400
 actcgggcag tgcaggtagc ttagcctctt ggtagctgcg gctttcaagg 450
 tgggccttgc cctggccgta gaagggattg acaagccga agatttcata 500
 ggcgatggct cccactgccc aggcattcagc cttgtgttag tcaatcactg 550
 cctgggggcc aggacgggcc gtggacacct gctcagaagc agtgggtgag 600
 acatcacgtc gcccgccat ctaacctttt catgtcctgc acatcacctg 650
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gottgagtga 700
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750
 acuggaactt cattctctg gaacatgagg gaacgcgga ggaaagcaaa 800
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850

gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900
 ggaagggtctg ccgatgggac atgacacact cgggaactcac ctctggggcc 950
 atcagacagc cgtttccgcc ccgatccacg taccagctgc tgaagggcaa 1000
 ctgcaggccg atgtctcat cagccaggca gcagccaaaa tctgcgatca 1050
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100
 ctccctctct tccctctgag aggcctctct atgtccctac taaagccacc 1150
 agcaagacat agctgacagg ggctaattgc tcagtgttgg ccaggagggt 1200
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacaaggaaa 1250
 tgcctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300
 ctcaatttaa atcatgttct agtaattgga gctgtccca agaccaaagg 1350
 agctagagct tggttcaaat gatctccaag ggccttata cccaggaga 1400
 ctttgatttg aatttgaaac cccaaatcca aacctaagaa ccagggtgat 1450
 taagaatcag ttattgcggg gtgtggtggc ctgtaatgcc aacattttgg 1500
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550
 gccacatgg tgaaacctct gtctctacta aaaatacaaa aaaactagcc 1600
 aggatggtg gtgtgtgct gtatcccagc tactcgggag gctgagacag 1650
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700
 ttccgctga gcaacacagc gagactctgt ctcaaaaaa ataaaaaaag 1750
 aattatgggt atttgtaa 1768

• 210 • 304

• 211 • 109

• 212 • PRT

• 213 • Homo sapiens

• 400 • 304

Met	Leu	Trp	Trp	Leu	Val	Leu	Leu	Leu	Pro	Thr	Leu	Lys	Ser
1				5				10					15

Val	Phe	Cys	Ser	Leu	Val	Thr	Ser	Leu	Tyr	Leu	Pro	Asn	Thr	Glu
				20				25						30

Asp	Leu	Ser	Leu	Trp	Leu	Trp	Pro	Lys	Pro	Asp	Leu	His	Ser	Gly
				35				40						45

Thr	Arg	Thr	Glu	Val	Ser	Thr	His	Thr	Val	Pro	Ser	Lys	Pro	Gly
				50				55						60

Thr	Ala	Ser	Pro	Cys	Trp	Pro	Leu	Ala	Gly	Ala	Val	Pro	Ser	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	65		70		75
Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala					
	80		85		90
Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly					
	95		100		105
Arg Arg Arg Asp					

02100 305
 02110 989
 02120 DNA
 02130 Homo sapiens

03000 305
 gggggggg gagtcgaga cctgtcccag gagctccagc tcacgtgacc 50
 tgtcaactgc tccgcgcgc tctgtccgc gccatgacc agccggtgcc 100
 ccggtctctc gtgcgcgcgc cgtgtgccc gggtccagcc gcactgggcg 150
 ccgcttcgc cactggctc ttctgggga ggcgtgccc cccatggcga 200
 ggcggcgag agcagtgc tttccccc gaggacagcc gctgtggca 250
 gtatctctc agccgtcca tggggagca ccgggcgtg cgaagcctga 300
 ggtgtgtgac cctggagcag ccgcagggg attctatgat gacctgcgag 350
 caggccagc tcttgccaa cctggcggg ctcctccagg ccaagaaggc 400
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 cgacctcgg ctgaagccc ccttgagac cctggacgag ctgctggcg 600
 cgggcgagg ccgcacctc gacgtggcc tgggtgatgc ggacaaggag 650
 aactgctcc cctactacg gcgtgctc cagctgctgc gaccggagg 700
 cctcctcgc gtctcagag tctgtggcg ccggaagggt ctgcaacctc 750
 cgaaagggga cgtggcgcc gactgtgtc gaaacctaaa cgaacgcctc 800
 ccggcgagc tcagggtcta ctcagctc ctgcccctgg gcgatggact 850
 caacctggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900
 gagggtgccc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306
 <211> 262
 <212> PFT
 <213> Homo sapiens

<400> 306

Met	Thr	Gln	Pro	Val	Pro	Arg	Leu	Ser	Val	Pro	Ala	Ala	Leu	Ala					
1				5					10					15					
Leu	Gly	Ser	Ala	Ala	Leu	Gly	Ala	Ala	Phe	Ala	Thr	Gly	Leu	Phe					
				20					25					30					
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys					
				35					40					45					
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser					
				50					55					60					
Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu					
				65					70					75					
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln					
				80					85					90					
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys					
				95					100					105					
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu					
				110					115					120					
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val					
				125					130					135					
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala					
				140					145					150					
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu					
				155					160					165					
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp					
				170					175					180					
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr					
				185					190					195					
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val					
				200					205					210					
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly					
				215					220					225					
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg					
				230					235					240					
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly					
				245					250					255					

Leu Thr Leu Ala Phe Lys Ile
260

02100 307
02110 2272
0212 DNA
0213 Homo sapiens

0400 307
ccgcgcgcgc agccgcctacc gccgcctgcag ccgccttccg cggcctgggc 50
ctctcgcgcgt cagcatgcc aacgccttca agcccgggga cttggtgttc 100
gctaagatda agggctacc tcactggcct gccaggatcg acgacatcgc 150
ggatgjcgc gtgaagcccc caccacaaca gtaccacata tttttcttj 200
gcacacacga aacagccttc ctgggaccca aggaactgtt cccctacgac 250
aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300
agggctgtgg gagatccaga acaaccccc cgcagctac agcgccctc 350
cgcagtgag ctctccgac agcgaggccc ccgaggccaa ccccgccgac 400
ggcagtgacg ctgaagagga cgatgaggac cggggggtca tggccgtcac 450
agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500
cagacaagag tagcacaac agtggcctga agaggaagac gctgcgccta 550
aaatgtcgg tctcjaaac agccccaaag gctccagcg acctggatca 600
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 <213> Homo sapiens

<400> 308
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	35	40	45
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro	50	55	60
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys	65	70	75
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala	80	85	90
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala	95	100	105
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp	110	115	120
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala	125	130	135
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser	140	145	150
Asp Asn Ser Gly Leu Lys Arg Lys Thr Pro Ala Leu Lys Met Ser	155	160	165
Val Ser Lys Arg Ala Arg Lys Ala Ser Ser Asp Leu Asp Gln Ala	170	175	180
Ser Val Ser Pro Ser Glu Glu Glu Asn Ser Glu Ser Ser Ser Glu	185	190	195
Ser Glu Lys Thr Ser Asp Gln Asp Phe Thr Pro Glu Lys Lys Ala	200	205	210
Ala Val Arg Ala Pro Arg Arg Gly Pro Leu Gly Gly Arg Lys Lys	215	220	225
Lys Lys Ala Pro Ser Ala Ser Asp Ser Asp Ser Lys Ala Asp Ser	230	235	240
Asp Gly Ala Lys Pro Glu Pro Val Ala Met Ala Arg Ser Ala Ser	245	250	255
Ser Ser Ser Ser Ser Ser Ser Ser Ser Asp Ser Asp Val Ser Val	260	265	270
Lys Lys Pro Pro Arg Gly Arg Lys Pro Ala Glu Lys Pro Leu Pro	275	280	285
Lys Pro Arg Gly Arg Lys Pro Lys Pro Glu Arg Pro Pro Ser Ser	290	295	300
Ser Ser Ser Asp Ser Asp Ser Asp Glu Val Asp Arg Ile Ser Glu	305	310	315
Trp Lys Arg Arg Asp Glu Ala Arg Arg Arg Glu Leu Glu Ala Arg			

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Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu Gln	
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Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg Gly	
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Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu Arg	
365	370	375
Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg Gly	
380	385	390
Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu Leu	
395	400	405
Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser Ser	
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Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val Arg	
425	430	435
Pro Glu Glu Lys Gln Gln Ala Lys Pro	Val Lys Val Glu Arg Thr	
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Arg Lys Arg Ser Glu Gly Phe Ser Met	Asp Arg Lys Val Glu Lys	
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Glu Ile Lys Phe Ala Leu Lys Val Asp	Ser Pro Asp Val Lys Arg	
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Cys Leu Asn Ala Leu Glu Glu Leu Gly	Thr Leu Gln Val Thr Ser	
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Gln Ile Leu Gln Lys Asn Thr Asp Val	Val Ala Thr Leu Lys Lys	
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Ile Arg Arg Tyr Lys Ala Asn Lys Asp	Val Met Glu Lys Ala Ala	
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Glu Val Tyr Thr Arg Leu Lys Ser Arg	Val Leu Gly Pro Lys Ile	
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575	580	585
Pro Gln Glu Lys Ala Glu Asp Lys Pro	Ser Thr Asp Leu Ser Ala	
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Pro Val Asn Gly Glu Ala Thr Ser Gln	Lys Gly Glu Ser Ala Glu	

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Asp Lys Glu His Glu Glu Gly Arg Asp	Ser Glu Glu Gly Pro Arg	
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Cys Gly Ser Ser Glu Asp Leu His Asp	Ser Val Arg Glu Gly Pro	
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Asp Leu Asp Arg Pro Gly Ser Asp Arg	Gln Glu Arg Glu Arg Ala	
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<211> 777

<212> PRT

<213> Homo sapiens

<400> 310

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Phe	Leu	Pro	Val	Thr	Gly	Thr	Leu	Lys	Gln	Asn	Ile	Pro	Arg	Leu	
				35					40					45	
Lys	Leu	Thr	Tyr	Lys	Asp	Leu	Leu	Leu	Ser	Asn	Ser	Cys	Ile	Pro	
				50					55					60	
Phe	Leu	Gly	Ser	Ser	Glu	Gly	Leu	Asp	Phe	Gln	Thr	Leu	Leu	Leu	
				65					70					75	
Asp	Glu	Glu	Arg	Gly	Arg	Leu	Leu	Leu	Gly	Ala	Lys	Asp	His	Ile	
				80					85					90	
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile	
				95					100					105	
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala	
				110					115					120	
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu	
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala	
				140					145					150	
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu	
				155					160					165	
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg	
				170					175					180	
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met	
				185					190					195	
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly	
				200					205					210	
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His	
				215					220					225	
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly	

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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
				260					265					270					
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
				275					280					285					
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Pip					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
				305					310					315					
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
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Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
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Lys	Glu	Ser	Ala	Asp	His	Arg	Trp	Val	Gln	Tyr	Asp	Gly	Arg	Ile					
				380					385					390					
Pro	Tyr	Pro	Arg	Pro	Gly	Thr	Cys	Pro	Ser	Lys	Thr	Tyr	Asp	Pro					
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Leu	Ile	Lys	Ser	Thr	Arg	Asp	Phe	Pro	Asp	Asp	Val	Ile	Ser	Phe					
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Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala					
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Gly	Gly	Pro	Thr	Phe	Lys	Arg	Ile	Asn	Val	Asp	Tyr	Arg	Leu	Thr					
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Gln	Ile	Val	Val	Asp	His	Val	Ile	Ala	Glu	Asp	Gly	Gln	Tyr	Asp					
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Val	Met	Phe	Leu	Gly	Thr	Asp	Ile	Gly	Thr	Val	Leu	Lys	Val	Val					
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Ser	Ile	Ser	Lys	Glu	Lys	Trp	Asn	Met	Glu	Glu	Val	Val	Leu	Glu					
				485					490					495					
Glu	Leu	Gln	Ile	Phe	Lys	His	Ser	Ser	Ile	Ile	Leu	Asn	Met	Glu					
				500					505					510					
Leu	Ser	Leu	Lys	Gln	Gln	Gln	Leu	Tyr	Ile	Gly	Ser	Arg	Asp	Gly					

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Cys Ala Asp Cys Cys Leu Ala Arg Asp Pro Tyr Cys Ala Trp Asp 545	550	555
Gly Asn Ala Cys Ser Arg Tyr Ala Pro Thr Ser Lys Arg Arg Ala 560	565	570
Arg Arg Gln Asp Val Lys Tyr Gly Asp Pro Ile Thr Gln Cys Trp 575	580	585
Asp Ile Glu Asp Ser Ile Ser His Glu Thr Ala Asp Glu Lys Val 590	595	600
Ile Phe Gly Ile Glu Phe Asn Ser Thr Phe Leu Glu Cys Ile Pro 605	610	615
Lys Ser Gln Gln Ala Thr Ile Lys Trp Tyr Ile Gln Arg Ser Gly 620	625	630
Asp Glu His Arg Glu Glu Leu Lys Pro Asp Glu Arg Ile Ile Lys 635	640	645
Thr Glu Tyr Gly Leu Leu Ile Arg Ser Leu Gln Lys Lys Asp Ser 650	655	660
Gly Met Tyr Tyr Cys Lys Ala Gln Glu His Thr Phe Ile His Thr 665	670	675
Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu 680	685	690
Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu 695	700	705
Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu 710	715	720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp 725	730	735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp 740	745	750
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<212> DNA

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> 212> DNA
> 213> Artificial Sequence

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> 223> Synthetic oligonucleotide probe

> 400> 312
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> 210> 313
> 211> 45
> 212> DNA
> 213> Artificial Sequence

> 220>
> 223> Synthetic oligonucleotide probe

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> 210> 314
> 211> 3934
> 212> DNA
> 213> Homo sapiens

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(210) 315
 (211) 370
 (212) PRT
 (213) Homo sapiens

(400) 315
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 1 5 10 15
 Val Phe Pro Pro Thr Pro Val Leu Cys Leu Pro Asn Gln Val Leu
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 Gln Arg Leu Glu Gln Arg Arg Gln Gln Ala Ser Glu Arg Glu Ala
 35 40 45
 Pro Ser Ile Glu Gln Arg Leu Gln Glu Val Arg Glu Ser Ile Arg
 50 55 60
 Arg Ala Gln Val Ser Gln Val Lys Gly Ala Ala Arg Leu Ala Leu
 65 70 75
 Leu Gln Gly Ala Gly Leu Asp Val Glu Arg Trp Leu Lys Pro Ala
 80 85 90
 Met Thr Gln Ala Gln Asp Glu Val Glu Gln Glu Arg Arg Leu Ser
 95 100 105
 Glu Ala Arg Leu Ser Gln Arg Asp Leu Ser Pro Thr Ala Glu Asp
 110 115 120
 Ala Glu Leu Ser Asp Phe Glu Glu Cys Glu Glu Thr Gly Glu Leu
 125 130 135
 Phe Glu Glu Pro Ala Pro Gln Ala Leu Ala Thr Arg Ala Leu Pro
 140 145 150

Cys Pro Ala His Val Val Phe Arg Tyr Gln Ala Gly Arg Glu Asp	155	160	165
Glu Leu Thr Ile Thr Glu Gly Glu Trp Leu Glu Val Ile Glu Glu	170	175	180
Gly Asp Ala Asp Glu Trp Val Lys Ala Arg Asn Gln His Gly Glu	185	190	195
Val Gly Phe Val Pro Glu Arg Tyr Leu Asn Phe Pro Asp Leu Ser	200	205	210
Leu Pro Glu Ser Ser Gln Asp Ser Asp Asn Pro Cys Gly Ala Glu	215	220	225
Pro Thr Ala Phe Leu Ala Gln Ala Leu Tyr Ser Tyr Thr Gly Gln	230	235	240
Ser Ala Glu Glu Leu Ser Phe Pro Glu Gly Ala Leu Ile Arg Leu	245	250	255
Leu Pro Arg Ala Gln Asp Gly Val Asp Asp Gly Phe Trp Arg Gly	260	265	270
Glu Phe Gly Gly Arg Val Gly Val Phe Pro Ser Leu Leu Val Glu	275	280	285
Glu Leu Leu Gly Pro Pro Gly Pro Pro Gln Leu Ser Asp Pro Glu	290	295	300
Gln Met Leu Pro Ser Pro Ser Pro Pro Ser Phe Ser Pro Pro Ala	305	310	315
Pro Thr Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly	320	325	330
Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro	335	340	345
Arg Leu Arg Pro Met Arg Pro Pro Pro Pro Pro Pro Ala Lys Ala	350	355	360
Pro Asp Pro Gly His Pro Asp Pro Leu Thr	365	370	

<210> 316
 <211> 4407
 <212> DNA
 <213> Homo sapiens

<400> 316
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aag:aaa 4407

0210 317

0211 837

0212 PRT

0213 Homo sapiens

0400 317

Met	Ser	Gln	Thr	Gly	Ser	His	Pro	Gly	Arg	Gly	Leu	Ala	Gly	Arg
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Trp	Leu	Trp	Gly	Ala	Gln	Pro	Cys	Leu	Leu	Leu	Pro	Ile	Val	Pro
			20						25					30

Leu	Ser	Trp	Leu	Val	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Ala	Ser	Leu
			35						40					45

Leu	Pro	Ser	Ala	Arg	Leu	Ala	Ser	Pro	Leu	Pro	Arg	Glu	Glu	Glu
			50						55					60

Ile	Val	Phe	Pro	Glu	Lys	Leu	Asn	Gly	Ser	Val	Leu	Pro	Gly	Ser
			65						70					75

Gly	Ala	Pro	Ala	Arg	Leu	Leu	Cys	Arg	Leu	Gln	Ala	Phe	Gly	Glu
			80						85					90

Thr	Leu	Leu	Leu	Glu	Leu	Glu	Gln	Asp	Ser	Gly	Val	Gln	Val	Glu
			95						100					105

Gly	Leu	Thr	Val	Gln	Tyr	Leu	Gly	Gln	Ala	Pro	Glu	Leu	Leu	Gly
			110						115					120

Gly	Ala	Glu	Pro	Gly	Thr	Tyr	Leu	Thr	Gly	Thr	Ile	Asn	Gly	Asp
			125						130					135

Pro	Glu	Ser	Val	Ala	Ser	Leu	His	Trp	Asp	Gly	Gly	Ala	Leu	Leu
			140						145					150

Gly	Val	Leu	Gln	Tyr	Arg	Gly	Ala	Glu	Leu	His	Leu	Gln	Pro	Leu
			155						160					165

Glu	Gly	Gly	Thr	Pro	Asn	Ser	Ala	Gly	Gly	Pro	Gly	Ala	His	Ile
			170						175					180

Leu	Arg	Arg	Lys	Ser	Pro	Ala	Ser	Gly	Gln	Gly	Pro	Met	Cys	Asn
			185						190					195

Val	Lys	Ala	Pro	Leu	Gly	Ser	Pro	Ser	Pro	Arg	Pro	Arg	Arg	Ala
			200						205					210

Lys	Arg	Phe	Ala	Ser	Leu	Ser	Arg	Phe	Val	Glu	Thr	Leu	Val	Val
			215						220					225

Ala	Asp	Asp	Lys	Met	Ala	Ala	Phe	His	Gly	Ala	Gly	Leu	Lys	Arg
			230						235					240

Tyr	Leu	Leu	Thr	Val	Met	Ala	Ala	Ala	Ala	Lys	Ala	Phe	Lys	His
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245	150	255
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260	265	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala		
275	280	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn		
290	295	300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu		
305	310	315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu		
320	325	330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys		
335	340	345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala		
350	355	360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys		
365	370	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val		
380	385	390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser		
395	400	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr		
410	415	419
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro		
425	430	435
Val Thr Phe Pro Gly Lys Asp Tyr Asp Ala Asp Arg Gln Cys Gln		
440	445	450
Leu Thr Phe Gly Pro Asp Ser Arg His Cys Pro Gln Leu Pro Pro		
455	460	465
Pro Cys Ala Ala Leu Trp Cys Ser Gly His Leu Asn Gly His Ala		
470	475	480
Met Cys Gln Thr Lys His Ser Pro Trp Ala Asp Gly Thr Pro Cys		
485	490	495
Gly Pro Ala Gln Ala Cys Met Gly Gly Arg Cys Leu His Met Asp		
500	505	510
Gln Leu Gln Asp Phe Asn Ile Pro Gln Ala Gly Gly Trp Gly Pro		
515	520	525
Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys Gly Gly Gly Val		

530	535	540
Gln Phe Ser Ser Arg Asp Cys Thr Arg	Pro Val Pro Arg Asn Gly	
545	550	555
Gly Lys Tyr Cys Glu Gly Arg Arg Thr	Arg Phe Arg Ser Cys Asn	
560	565	570
Thr Glu Asp Cys Pro Thr Gly Ser Ala	Leu Thr Phe Arg Glu Glu	
575	580	585
Gln Cys Ala Ala Tyr Asn His Arg Thr	Asp Leu Phe Lys Ser Phe	
590	595	600
Pro Gly Pro Met Asp Trp Val Pro Arg	Tyr Thr Gly Val Ala Pro	
605	610	615
Gln Asp Gln Cys Lys Leu Thr Cys Gln	Ala Arg Ala Leu Gly Tyr	
620	625	630
Tyr Tyr Val Leu Glu Pro Arg Val Val	Asp Gly Thr Pro Cys Ser	
635	640	645
Pro Asp Ser Ser Ser Val Cys Val Gln	Gly Arg Cys Ile His Ala	
650	655	660
Gly Cys Asp Arg Ile Ile Gly Ser Lys	Lys Lys Phe Asp Lys Cys	
665	670	675
Met Val Cys Gly Gly Asp Gly Ser Gly	Cys Ser Lys Gln Ser Gly	
680	685	690
Ser Phe Arg Lys Phe Arg Tyr Gly Tyr	Asn Asn Val Val Thr Ile	
695	700	705
Pro Ala Gly Ala Thr His Ile Leu Val	Arg Gln Gln Gly Asn Pro	
710	715	720
Gly His Arg Ser Ile Tyr Leu Ala Leu	Lys Leu Pro Asp Gly Ser	
725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu	Met Pro Ser Pro Thr Asp	
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu	Arg Tyr Ser Gly Ala Thr	
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His	Gly Pro Leu Ala Gln Pro	
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly	Asn Pro Gln Asp Thr Arg	
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg	Pro Thr Pro Ser Thr Pro	
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His	Arg Arg Ala Gln Ile Leu	

815

820

825

Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys
830 835

<210> 318

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 318

ccctgaagct gccagatggc tcc 23

<210> 319

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 319

ctgtgtcttt cggtgcagcc agtc 24

<210> 320

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 320

cccaagatgt ggtactgct ggggcagtc gcttgcgcta cag 43

<210> 321

<211> 1197

<212> DNA

<213> Homo sapiens

<400> 321

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ttgtggactg gtgttttgta tcttggccct aactctaatt gtctgtttt 200

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(210) 322

(211) 317

(212) PET

(213) Homo sapiens

(400) 322

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Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys
				20				25						30
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val
				35				40						45
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys
				50				55						60
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys
				65				70						75
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe

80										85					90				
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe					
				95					100					105					
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys					
				110					115					120					
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro					
				125					130					135					
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe					
				140					145					150					
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn					
				155					160					165					
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn					
				170					175					180					
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu					
				185					190					195					
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala					
				200					205					210					
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro					
				215					220					225					
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu					
				230					235					240					
Glu	Gln	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe					
				245					250					255					
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg					
				260					265					270					
Arg	Gly	Asn	Arg	Tyr	Cys	Arg	Arg	Val	Cys	Glu	Pro	Leu	Leu	Gly					
				275					280					285					
Tyr	Tyr	Pro	Tyr	Pro	Tyr	Cys	Tyr	Gln	Gly	Gly	Arg	Val	Ile	Cys					
				290					295					300					
Arg	Val	Ile	Met	Pro	Cys	Asn	Trp	Trp	Val	Ala	Arg	Met	Leu	Gly					
				305					310					315					

Arg Val

<210> 313

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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<210> 324
 <211> 249
 <212> PRT
 <213> Homo sapiens

<400> 314
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 Leu Gly Met Val Gly Thr Leu Ile Thr Thr Ile Leu Pro His Trp

	20	25	30
Arg Arg Thr Ala His Val Gly Thr Asn Ile Leu Thr Ala Val Ser	35	40	45
Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly	50	55	60
Ile Tyr Gln Cys Gln Ile Tyr Arg Ser Leu Leu Ala Leu Pro Gln	65	70	75
Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu	80	85	90
Ser Gly Ile Ala Cys Ala Cys Ala Val Ile Gly Met Lys Cys Thr	95	100	105
Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu	110	115	120
Gly Gly Thr Leu Phe Ile Leu Ala Gly Leu Leu Cys Met Val Ala	125	130	135
Val Ser Trp Thr Thr Asn Asp Val Val Gln Asn Phe Tyr Asn Pro	140	145	150
Leu Leu Pro Ser Gly Met Lys Phe Glu Ile Gly Gln Ala Leu Tyr	155	160	165
Leu Gly Phe Ile Ser Ser Ser Leu Ser Leu Ile Gly Gly Thr Leu	170	175	180
Leu Cys Leu Ser Cys Gln Asp Glu Ala Pro Tyr Arg Pro Tyr Gln	185	190	195
Ala Pro Pro Arg Ala Thr Thr Thr Thr Ala Asn Thr Ala Pro Ala	200	205	210
Tyr Gln Pro Pro Ala Ala Tyr Lys Asp Asn Arg Ala Pro Ser Val	215	220	225
Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val	230	235	

<210> 325

<211> 2121

<212> DNA

<213> Homo sapiens

<400> 325

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(210) 326
 (211) 261
 (212) PFT
 (213) Hemo sapiens

(400) 326
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 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp
 20 25 30
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln
 35 40 45
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe
 50 55 60
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met
 65 70 75
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly
 80 85 90
 Ala Ile Gly Leu Leu Val Ser Ile Phe Ala Leu Lys Cys Ile Arg
 95 100 105
 Ile Gly Ser Met Glu Asp Ser Ala Lys Ala Asn Met Thr Leu Thr
 110 115 120
 Ser Gly Ile Met Phe Ile Val Ser Gly Leu Cys Ala Ile Ala Gly
 125 130 135
 Val Ser Val Phe Ala Asn Met Leu Val Thr Asn Phe Trp Met Ser
 140 145 150

Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val
				155				160					165	
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val
				170				175					180	
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala
				185				190					195	
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser
				200				205					210	
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe
				215				220					225	
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile
				230				235					240	
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro
				245				250					255	
Ser	Lys	His	Asp	Tyr	Val									
				260										

<210> 327

<211> 3010

<212> DNA

<213> Homo sapiens

<400> 327

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 tccctgctgg ctctttctcc ggacctacag gcagccagag gaactgatgtg 350
 tcttgcttcc gtgatgtcct tcttggcttt catgatggcc atccttgcca 400
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<210> 328

0120 PFT

4400: 328

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35 40 45

Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
50 55 60

Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
65 70 75

Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
80 85 90

Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
35 100 105

Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
110 115 120

Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
135 139 135

Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
148 149 150

Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
155 160 165

Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
170 175 180

Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
135 190 195

Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
200 205 210

Thr Gly Lys Lys Ser Pro Ser Val Tyr Ser Arg Ser Gln Tyr Val
215 220 225

· 211 · 13:15

213. Homo sapiens

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<210> 330
 <211> 220
 <212> PRT
 <213> Homo sapiens

<400> 320

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              20              25              30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
              35              40              45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
              50              55              60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
              65              70              75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
              80              85              90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
              95              100              105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
              110              115              120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
              125              130              135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
              140              145              150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
              155              160              165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
              170              175              180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
              185              190              195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
              200              205              210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
              215              220

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<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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<210 - 332

<211 - 173

<212 - PRT

<213 - Homo sapiens

<400 - 332

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Tyr	Ser	Ser	Leu	Leu	Ala	Leu	Pro	Pro	Ala	Leu	Glu	Thr	Ala	Arg
			20						25				30	
Ala	Leu	Met	Cys	Val	Ala	Val	Ala	Leu	Ser	Leu	Ile	Ala	Leu	Leu

35	40	45
Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
50	55	60
Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
65	70	75
Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
80	85	90
Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
95	100	105
Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
110	115	120
Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
125	130	135
Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
140	145	150
Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
155	160	165
Ser Lys Thr Ser Thr Ser Tyr Val		
170		

<210> 333

<211> 535

<212> DNA

<213> Homo sapiens

<400> 333

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agaagtatcc agtggtyggc atccctggc ccatacata cctaccagtt 200
tgtggtttctg actacatcac ctatgggaat gaatgtcact tgtgtaocga 250
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tcatacacc aggtctctgac tgagtttctt tcagttttac tgatgtttctg 400
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tttttaacac gtcaataaaa aaataatctc ccaga 535

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<210> 334
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 334
 Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
 1 5 10 15

 Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
 20 25 30

 Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
 35 40 45

 Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
 50 55 60

 Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
 65 70 75

 Arg Val Gln Phe Leu His Asp Gly Ser Cys
 80 85

<210> 335
 <211> 742
 <212> DNA
 <213> Homo sapiens

<400> 335
 cccgcgcgcgcg gttctccctc gcagcaccctc gaagtgcgcgc cctgcgcctc 50

 ctgttcgcgcg cccgcgcgcga tggctgcctc cccgcgcgcgc cctgcctgtcc 100

 tggcctctgac cgggctggcg ctgctcctgc tccctgtgtg gggcccaggt 150

 ggcataagtg gaaataaact caagctgatg cttcaaaaaa gagaagcacc 200

 tgttccaaact aagactaaag tggcgcgttg tgagaataaa gccaaaagaat 250

 tcccttggcag cctgaagcgc cagaagcgcgc agctgtggga cccgactcgg 300

 cccgcaggtgc agcagtggtc ccagcagttt ctctacatgg gctttgatga 350

 agcgaatttt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

 gactgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

 gcaatttggtc cccgcgcgcgc ctaaggcttt aggcctggag ccagcgtcaa 500

 ctacgatgac tactaaccat gaactgcac acgctgtaca agaagcaaat 550

 agcgattctc ttcagtgtat tccaatgccc ttacactact tggttttctga 600

 tttgtcttat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650

 gaaaggttaa aacaacacat gtaaatgcct tttgatattt catgggaatg 700

cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336

<211> 148

<212> PRT

<213> Homo sapiens

<400> 336

Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
1 5 10 15

Leu Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
20 25 30

Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
35 40 45

Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
50 55 60

Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
65 70 75

Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
80 85 90

Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
95 100 105

Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
110 115 120

Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
125 130 135

Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
140 145

<210> 337

<211> 1310

<212> DNA

<213> Homo sapiens

<400> 337

gggtctgaga ccgcccggaa gtgcccagg ggcggcgatg gagctggggg 50

agccgggggc tgggtagcgc ggccgggcaag gcaggcgcca tgacctgat 100

tgaaggggtg ggtgatgagg tgaccgtcct ttctcgggtg cttgcctgac 150

ttctgggtgc ggcccttgcc tgggtctcaa cgcacacgc tgaggggggg 200

gaaccactgc ccagccgtc agggacccca acccatccc agccagcgc 250

agccatggca gctaccgaca gcatgagagg ggaggccca ggggcagaga 300

ccccagcct gagacacaga ggtcaagctg cacagccaga gccacagcag 350
gggttcacag caacaccgcc agcccggac tcccgcagg agcccctgt 400
gctacggctg aaattctca atgattcaga gcaggtggcc agggcctggc 450
cccacgacac cattggctcc ttgaaaagga cccagtctcc cggccgggaa 500
cagcaggtgc gactcatcta ccaagggpag ctgctaggcg acgacaccca 550
gacccctgggc agccttcacc tccctcccaa ctgcgttctc cactgccaag 600
tgtccacpag agtcggtccc ccaaatccc cctgcccgcg ggggtccag 650
ccgggcccct cggggctgga aatcggcagc ctgctgctgc cctgctgct 700
ctgctgcttg ctgctgctct ggtactgcca gatccagtae cggcccttct 750
ctccctgac cgcactctg ggcctggccg gcttcacct gctcctcagt 800
ctcctggcct ttgcctgta ccgcccgtag tgcctccgcg gggcttggc 850
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ctgctgccc aggcccgcct ctccggcctg cctcttcccg ctgcccctga 950
gcccagccct ggcccgcaga ggactcccgc gactggcgga ggccccgccc 1000
tgccacccc ggggtccggg gccacctccc ggggtgctg aacctcagcc 1050
tgactggga gtgggtcctt cgggtccggg catctgctgt cgtgcccctg 1100
gcccgggga gagccgggga gcccggggg ccggtcttag tgtctctgag 1150
gaggacccag cgcctccaa tccctgacag ctccctgggc tgagttgggg 1200
acgcccagtc ggtgggagga tggggaagg gagccgggag gggcagagga 1250
gttcccggga acccgtgag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
aaaaaaaaa 1310

(110) 338
(111) 246
(112) PRT
(113) Homo sapiens

(140) 338
Met Thr Leu Ile Glu Gly Val Gly Asp Glu Val Thr Val Leu Phe
1 5 10 15
Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser
20 25 30
Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly
35 40 45

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Ser	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
His	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

(210) 339

(211) 349

(212) DNA

(213) Homo sapiens

(400) 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

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caagacccta agaaccatca ggcctcaggt gcacctctc cctccaagg 150

atgacaaagg cgtactcat ctatttggtc agcagtttc ttgcctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccagggt ctgcagctgg 250

aggacttggg tgggtttgag gggtactccc tgagtgaactg gctgtgcoctg 300
 gctttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tgggaagcttt gactatggcc ttttcagat caaagccac tactggtgca 400
 acgattataa gagttactcg gaaaacottt gccacgtaga ctgtcaagat 450
 ctgctgaatc ccaacottct tgcaggcatc cactggcgaa aaaggattgt 500
 gtcgggagca cgggggatga acaactgggt agaattggagg ttgcactggt 550
 caggccggcc actctctac ttgctgacag gatgcggcct gagatgaaac 600
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 ggattcttca tttctcttc ctactgctc cacttcattgt tttttcttc 700
 ccttcccatt tacaactaaa actgaccaga gccacaggaa taaatgggtt 750
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 tgttatttgt aaactgagga ccacaataaa gaaatcttta ttttatcg 849

(210) 340
 (211) 148
 (212) PRT
 (213) Homo sapiens

(400) 340
 Met Thr Lys Ala Leu Leu Ile Tyr Leu Val Ser Ser Phe Leu Ala
 1 5 10 15
 Leu Asn Gln Ala Ser Leu Ile Ser Arg Cys Asp Leu Ala Gln Val
 20 25 30
 Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser
 35 40 45
 Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser
 50 55 60
 Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe
 65 70 75
 Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser
 80 85 90
 Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn
 95 100 105
 Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala
 110 115 120
 Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly
 125 130 135

Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg
140 145

<210> 341

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

gcctcraagg atgacaaagg cgc 23

<210> 342

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 342

gttcagcagc tttcttgccc taaatcagg 29

<210> 343

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 343

atctcaggcg gcatactgtc agcc 24

<210> 344

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

gttgatgact gcaagaaggt tggg 24

<210> 345

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 345

agctttcttg cccataatca ggcacagctc atcagtcgct gtgac 45

(210) 346

(211) 2575

(212) DNA

(213) Homo sapiens

(400) 346

tctgacctga ctggaagcgt ccaaaagagg acgctgtgca gccctgcttg 50

actgagaacc caccagctca tcccagacac ctcatagcaa cctatttata 100

caaaggggga aagaaacaac tgagcagaat ggaatcatta tttttttccc 150

aaggagaaaa ccgggggtaaa gggagggaag caattcaatt tgaagtccct 200

gtgaatgggc tttcagaagg caattaaaga aatccactca gagaggactt 250

gggggtgaac ttgggtccctg tggttctctg attgtaagtg gaagcaggto 300

ttgcacacgc tgttggcaaa tgtcaggacc aggttaagtg actggcagaa 350

aaacttcag gtggaacaag caaccatgt tctgtgcga gcttgaagga 400

gcttgagcg ggagaaagct aactgaaca tgacctgttg catttggcaa 450

gttctagcaa catgtctcta aggaagcgat acaggcacag accatgcaga 500

ctccagttcc tctgtctgtt cctgatgctg ggatggctcc tgatgatggt 550

ggcgatgttg caacctcccc accacacct gcaccagact gtcacagccc 600

aagtcagcaa gcacagacct gaagccaggt accgcttggc ctctggggaa 650

tcccaaggatt gggtaactgga agctgaggat gagggtgaag agtacagccc 700

tctggagggc ctgcacacct ttatctcact gggggaggat cagctgctgg 750

tggcctgtggc cttaccacag gccagaagga accagagcca gggcaggaga 800

ggtgggagct accgcttcac caagcagcca aggaggcagg ataagggaagc 850

ccaaaagagg gactgggggg ctgatgagga cggggaggtg tctgaagaag 900

aggagttgac cccgttcagc ctggacccac gtggcctcca ggaggcactc 950

agtgcacgca tccccctcca gagggtcttg cccgaggtgc ggcacccact 1000

gtgtctgcag cagcacctc aggacagctt gccacagcc agcttcactc 1050

tctgtttcca tgatgaggcc tggccactc tctggggac tgtacacagc 1100

atctctgaca cagtgcacag ggccttcttg aaggagatca tctctgtgga 1150

cgacctcagc cagcaaggac aactcaagtc tgcctcagc gaatatgtgg 1200

ccaggctgga ggggggtgaag ttactcagga gcaacaagag gctgggtgac 1250

atcaggggccc ggatgctggg gccaccaga gccacgggg atgtgctcgt 1300
 ctccatggat gccactggc agtgccacc aggtggtgtg gagccctcc 1350
 tcagcagaat agctggtgac aggagccgag tggatatctc ggtgatagat 1400
 gtgattgact ggaagacttt ccagtattac cctccaaagg aactgcagcg 1450
 tgggtgtgtg gactggaagc tggatttcca ctgggaacct ttgccagagc 1500
 atgtgaggaa ggcctccag tccccataa gccccatcag gagccctgtg 1550
 gtgcccggag aggtggtggc catggacaga cattacttcc aaaaacactg 1600
 aggttatgac tctcttatgt cgtgcgagg tggtgaaaaa ctgaaactgt 1650
 ctttcaaggc ctggctctgt ggtggctctg ttgaaacct tccctgtct 1700
 cgggtaggac acatctacca aaatcaggat tccattccc ccttcgacca 1750
 gga gccacc ctgaggaaca ggttcgcac tgcagagacc tggctgggt 1800
 cctccaaaga aacctctac aagcatagcc cagaggcctt ctcttgagc 1850
 aagctgaga agccagactg catggaacgc ttgcagctgc aaaggagact 1900
 ggggtgtcgg acattccact ggtttctggc taatgtctac cctgagctgt 1950
 acccatctga acccaggccc agtttctctg gaaagctcca caaacctgga 2000
 cttggctct gtgcagactg ccaggcagaa ggggacatcc tgggtgtcc 2050
 catggtgttg gctccttgca gtgacagccg gcagcaacag taactgcagc 2100
 acaccagcag gaaggagatt cactttggca gccacagca cctgtgcttt 2150
 gctgtccaggc aggagcaggt gattcttcag aactgcacgg aggaaggcct 2200
 ggcacccac cagcagcact gggacttcca ggagaatggg atgattgtcc 2250
 acattctttc tgggaaatgc atggaagctg tggtgcaaga aaacaataaa 2300
 gatttgtaac tgcgtccgtg tgatggaaaa gcccgccagc agtggcgatt 2350
 tgaccagata aatgctgtgg atgaacgatg aatgtcaatg tcagaaggaa 2400
 aagagaatth tggccatcaa aatccagctc caagtgaacg taaagagctt 2450
 atatatctca tgaagctgat ccttttgtgt gtgtgtctct tgtgttagga 2500
 gagaaaaaag ctctatgaaa gaatatagga agtttctctt ttccacacct 2550
 tatttcattg actgctggct gctta 2575

<210> 347

<211> 639

(212) PRT

(213) Homo sapiens

(400) 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln	
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val	
				20					25					30	
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr	
				35					40					45	
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp	
				50					55					60	
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly	
				65					70					75	
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu	
				80					85					90	
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg	
				95					100					105	
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile	
				110					115					120	
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp	
				125					130					135	
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr	
				140					145					150	
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala	
				155					160					165	
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu	
				170					175					180	
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val	
				185					190					195	
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr	
				200					205					210	
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu	
				215					220					225	
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser	
				230					235					240	
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu	
				245					250					255	
Arg	Ser	Asn	Lys	Arg	Leu	Gly	Ala	Ile	Arg	Ala	Arg	Met	Leu	Gly	
				260					265					270	

Ala Thr Arg Ala Thr Gly Asp Val Leu Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His Pro Gly Trp Leu Glu Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg Ser Arg Val Val Ser Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr Phe Gln Tyr Tyr Pro Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp Trp Lys Leu Asp Phe His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg Lys Ala Leu Gln Ser Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val Pro Gly Glu Val Val Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr Gly Ala Tyr Asp Ser Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu Glu Leu Ser Phe Lys Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile Leu Pro Cys Ser Arg Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser His Ser Pro Leu Asp Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg Ile Ala Glu Thr Trp Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys His Ser Pro Glu Ala Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp Cys Met Glu Arg Leu Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr Phe His Trp Phe Leu Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser Glu Pro Arg Pro Ser Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu Gly Leu Cys Ala Asp Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys Pro Met Val Leu Ala Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr Leu Gln His Thr Ser Arg Lys Glu Ile His Phe	545	550	555

Gly	Ser	Pro	Gln	His	Leu	Cys	Phe	Ala	Val	Arg	Gln	Glu	Gln	Val
				560					565					570
Ile	Leu	Gln	Asn	Cys	Thr	Glu	Glu	Gly	Leu	Ala	Ile	His	Gln	Gln
				575					580					585
His	Trp	Asp	Phe	Gln	Glu	Asn	Gly	Met	Ile	Val	His	Ile	Leu	Ser
				590					595					600
Gly	Lys	Cys	Met	Glu	Ala	Val	Val	Gln	Glu	Asn	Asn	Lys	Asp	Leu
				605					610					615
Tyr	Leu	Arg	Pro	Cys	Asp	Gly	Lys	Ala	Arg	Gln	Gln	Trp	Arg	Phe
				620					625					630
Asp	Gln	Ile	Asn	Ala	Val	Asp	Glu	Arg						
				635										

<210> 348

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 348

gacaggtgg tggccatgga cag 23

<210> 349

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 350

tatgtgcgtg cgagggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351

<211> 2324

<212> DNA

<213> Homo sapiens

<400> 351

cgccaagcat gcagtaaaag ctqaaaatct qggtcacagc tgaggaagac 50
ctcagacatg gaggccagga tglggootgc gctgctgctg tcccacctcc 100
tccctctctg gccactcttg ttgttgcccc tcccacogcc tgcctagggc 150
tcttcatctc cccctcgaa cccaccagcc ccagccogcc cccctgtgtg 200
caggjgaggg cctctggccc cacttcctgt gctgctgtgg gagcgagcac 250
ctccaccaag ccgatctctt cgggtcccaa gatacgtcg gcaagtcctg 300
cctggaactg cacccccagc caccctatca ggttttgagg aggggcccgc 350
ctcattccaa taacctgagg ctatctgttg ggttcccaac gtgtctcgag 400
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tttgagagcc ctcatgggct cgcaccccca caccccaact cagaactcat 500
ggagagtgat ggagatgggc ttatctctgg agaggcaact gccacctgc 550
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agcaaggtgc cctgaggcag gaggagagcc agcagccact gacagacctg 750
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caccctcgac catgaggagc ccgagggggg accccggcct gggatgccc 850
accccaaggg ggcctcagcc ttccagttga accggtgagg gcaggggcaa 900
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gcccctggcc ctcccaaggg ggcctggaca gctctctctt gggaggcaac 1050
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caactctgcc ctcttaact tgattcccc tctttgtctt gaacttccc 1200
tctattctg gctacccc ttgttctga ctgtgcctt tccctcttc 1250
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cacaccaccc ggaacactcc ccagcccccac gggcaatcct atctgctcgc 1450
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 cacccttggtg cactcacatg aaagccttgc acactcacct ccacottcac 1550
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 tcagctgact ctcatgttct ctctctccac atttgcactc tctccttccc 1650
 acattctgtg ctacgctcac tcagtgggta gcggtttcctg cacactttac 1700
 ctctcatgtg cgtttccggg cctgatgttg tgggtgggtg agggctgctc 1750
 actctctccc tcctgaacac ccacccacct cgtttccgca gccctggct 1800
 gctgctccag aggtgggtgg gaggtgagct gggggctcct tgggcccctc 1850
 tcgggtcatgg tctcgtccca ttccacacca ttgtttctc tgtctcccca 1900
 tccctactca aggatgcggg catcacctg agggctcccc ctggggaatg 1950
 gggtagtgag gccccagact tcaccccccag ccacgtgcta aaatctgttt 2000
 tctgacagat ggggttttgg gagtcgctg ctgcactaca tgagaaaggg 2050
 actcccattt gcccttccct ttctctaca gtcccttttg tcttgtctgt 2100
 cctggctgtc tgtgtgtgtg ccattctctg gacttcagag cccctgagc 2150
 cagtcctccc ttcccagcct ccccttgggc ctccctaaat ccacctagga 2200
 tggcagggac cggagtccgc tggttcaagg ccctcgggag cctgctccc 2250
 aagtctaccc ttcccttccc ggactccctc ctgtccctc cttctcctcc 2300
 tccctccttc cactctctt ccttttgctt ccttgccctt tccctctcct 2350
 caggttcttc cctccttctc actggttttt ccaccttctt ccttcccttc 2400
 ttccctgggt cctaggctgt gatatatatt ttgtattat ctctttcttc 2450
 ttcttgtggt gatcatctg aattactgt ggatgtaagt tccaaaattt 2500
 tccaaataaag cctttgcaag ataa 2524

<210> 352
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 352
 Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
 1 5 10 15
 Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
 20 25 30

Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	35	40	45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	50	55	60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	65	70	75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	80	85	90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Gln	Ser	Trp	Thr	Pro	Asn	95	100	105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	110	115	120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	125	130	135
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240
Leu Pro Lys																	

<210> 353
 <211> 480
 <212> DNA
 <213> Homo sapiens

<400> 353
 gtttaaccagc gaagtcctcc gtgggtcccg cccgcgcgtg cctcactcc 50
 aggcacggat ggcattctgt ctggccctgc gcattggcgt gctgctggtc 100
 tccggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150

cgtgccacg ctgtggaag agccggccga gctgcccgtg ggagaaggcc 200
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggcccccca 250
 gcccccacgg tcggcgccag acccgaggac agcacccggc aggagccggt 300
 ggaccagggc ggccgggtgc tggggcccgg cgttatcgcg gccatcgtga 350
 tcggcgccct gctggccacc tgggtggtgc tggcgctcgt ggtcgtcgcg 400
 ctgagaaagt tttctgcctc ctgaagcgaa taaaggggac ggcgcgggac 450
 gggcgcgac tcggcaaaaa aaaaaaaaaa 480

#210 - 354

#211 - 121

#212 - PFT

#213 - Homo sapiens

#400 - 354

Met	Ala	Ser	Cys	Leu	Ala	Leu	Arg	Met	Ala	Leu	Leu	Leu	Val	Ser
1				5				10					15	
Gly	Val	Leu	Ala	Pro	Ala	Val	Leu	Thr	Asp	Asp	Val	Pro	Gln	Glu
				20				25					30	
Pro	Val	Pro	Thr	Leu	Trp	Asn	Glu	Pro	Ala	Glu	Leu	Pro	Ser	Gly
				35				40					45	
Glu	Gly	Pro	Val	Glu	Ser	Thr	Ser	Pro	Gly	Arg	Glu	Pro	Val	Asp
				50				55					60	
Thr	Gly	Pro	Pro	Ala	Pro	Thr	Val	Ala	Pro	Gly	Pro	Glu	Asp	Ser
				65				70					75	
Thr	Ala	Gln	Glu	Arg	Leu	Asp	Gln	Gly	Gly	Gly	Ser	Leu	Gly	Pro
				80				85					90	
Gly	Ala	Ile	Ala	Ala	Ile	Val	Ile	Ala	Ala	Leu	Leu	Ala	Thr	Cys
				95				100					105	
Val	Val	Leu	Ala	Leu	Val	Val	Val	Ala	Leu	Arg	Lys	Phe	Ser	Ala
				110				115					120	

Ser

#210 - 355

#211 - 2134

#212 - DNA

#213 - Homo sapiens

#400 - 355

ggcgttggt tgggtggcgg ctgaagggtg tggcgcgagc agcgtcgttg 50
 gttggcggc ggcggggcgg gacgggcatg gccctgctgc tgtgcctggt 100

gtgcctgacg ggggcgctgg cccacggctg totgcactgc cacagcaact 150
 tctccaagaa gttctccttc tacgcgcaac atgtgaaact caagtcctgg 200
 tgggtggggc acatccccgt gtcaggggcg ctgctcaccg actggagaga 250
 cgacacgatg aaggagctgc aactggccat ccccgccaag atcacccggg 300
 agaagctgga ccaagtggcg acagcagtg accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggttat ttcccacaag agctgggaaa 400
 catcttcggg gagcaggtgc aactcatcca gaacgcacac atcgaaaggc 450
 aactggcacc aggcagctgg ggaggagggc agctctccag ggagggaacc 500
 agcctagcac ctgaaggatc aatgcaccca ccccgggggg aactccctca 550
 agtagccccc agaggcgctg ggagtgttgc caccgacctc cctgaagtt 600
 tgcctccatc cagctggggg gtcaacctgg ggaccttc cctccgggac 650
 atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
 tggcatcttc cagtaagaga ccctctctcg caacaaactgc acagaactgc 750
 acgtcgctcg ctttggtat aactggagat agggctcagg catcacaccc 800
 acccgtgcca gggccctact gtccctgggg tcccaggctc ccttgaggag 850
 gggctccccg ccttcacact ggtgtcacc ggttagggcg gggccgtggg 900
 ttcagggcg caccacttc aagcctgtgt cccacaggtc ctgggcgcag 950
 tggaagtcag ctgtccaggg cctcctgaac tacataaata actggcaca 1000
 gtaagtcccc tctcaaac aacacaggca gtgtgtgtat gtgagcaact 1050
 cgtgggtgag tatgtgtgg gcacaggctg gctccctcag ctcccacgtc 1100
 ctgagggggc tcccaggag gtggaaactc aaccagctc tgccaggag 1150
 gggctgcag tcttttctc cctcaaaagt ctccgacct cagctggagg 1200
 cgggcactct tctaaaggg tcccacagg gtctgttcc accccatccc 1250
 aggtctgtgg tcagagcctg ggagggttcc ctacgatgt taggggtgac 1300
 ccattggagg gctgactgac ccacattgac ttccagacag gacacgagca 1350
 tgaggtaagg ccgcctgac ctggacttca gggggagggg gtaaaggag 1400
 agaggagggg ggtaggggg tctctagat cagtggggc actgcaggtg 1450
 gggctctccc tatacctggg acacctgct gatgtcact ctgcaaccac 1500

acccatgtgg tggtttcacg aacagaccac gctctctctg cttctctctg 1550
 cctggggacac acagagccac cccggccttg tgagtgaacc agagaaggga 1600
 ggctctggga gaaggggtgc tctgaagcca acaccaggtt gcggcggcct 1650
 gcacacccct cggacatccc aggcacgagg gtgtctgtga tgtggccaca 1700
 cataggacca caagtcaccg ctgggaggag aggcctgggg cccccaggga 1750
 aggaggcagg ggggtggggga catggagaga tgaggcagcc tctctctccc 1800
 gcagcctggt atgcacagcc ttaaggtgtc tggagccccc acaattgggc 1850
 aacctgacct tgggaagatgc tcttgagtgt ctcaagcagc actgacagca 1900
 gctgggcctg ccccaggcca acgtgggggc ggagaactcag ctggacagcc 1950
 cctgcctgtc actctggagc tgggtgtgtc ctgcctcagg accccctctc 2000
 cgaccccggg cagagctgag ctggccaggc ccaggagggc gggagggagg 2050
 gaatgggggt ggggtgtgtc cagcatcagc gctggggcag gtcgcagag 2100
 ctgggggatg tgattaaagt cctgatggt tctc 2134

#210 - 356
 #211 - 157
 #212 - FET
 #213 - Homo sapiens

#400 - 356
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
 1 5 10 15
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln

125

130

135

Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro
 140 145 150

Ser Pro Arg Gly Asp Leu Pro
 155

(C110): 357

(C111): 1536

(C112): DNA

(C113): Homo sapiens

(C400): 357

agcaggagca ggagagggac aatggaagct gcccggtcba ggttcattgtt 50
 cctcttatttt ctcttcacgt gtgagctggc tgcagaagtt gctgcagaag 100
 ttgagaaaac ctccagatggc cctgggtgctg cccaggaaac caagtggctc 150
 acaagatgtcc cagctgcccatt ggaattccatt gctgcacactg aggtgggtgt 200
 catagggcttc ttccaggatt tagaaatacc agcagtgccc ataactccata 250
 gcctgggtgca aaaattccca gggtgtctat ttgggatacag caactgattct 300
 gaggtttctga cacaactacaa cctcactggg aacacccatct gctctttctg 350
 ccttggtagac aatgaacaac tgaattttaga ggaaggaagac attgaaagca 400
 ttgatgcac caaattgagc cgttttcattg agatcaacag cctccacatg 450
 gtgacagagt acaacccgtg gactgtgatt gggctattca acagcgtaat 500
 ccagattcat ctctctctga taatgaacaa ggctccccc gagtatgaag 550
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
 ctcttttattc tgggtgacag tggatatgaa gaaaatggga aggtgatata 650
 atttttcaaa ctaaaaggagt ctcaactgcc agcttttggca atttaccaga 700
 ctctagatga cgagtgggat acactgcccc cagcagaagt ttccgttagag 750
 catgtgcaaa acttttgtga tggattccta agtggaaaaat tgttgaaaga 800
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaaactc tgaattctcc 850
 ttggaaactac atatggccaa gtatctactt tatgcacagt aaaaaggcac 900
 aactcaaatc tcagagacac taaacaacag gatcactagg cctgcacacc 950
 acacacacac gcaagtgcac acaagcagc abggtgcac acacacacgc 1000
 gacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
 tctcttcttc ctctctttta atttccatc ctcaactccct atccaatttc 1100

atttattatcg tgcattcata ctctgtaagc ccattctgtaa cacacctaga 1150
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200
 cttagagaaag attgttccaa ttgttcattt aatatcaagt ttgtatactg 1250
 cacatgactt acacacacaa tagttctctg tcttttaagg ttacctaaagg 1300
 gttgaaactc taccttcttt cataagcaca tgttcgtctc tgaactcagga 1350
 tcaaaaaacca aaggatgggt ttaaaccact ttgtgaaatt gtctttttgc 1400
 cagaagttaa aggtgtctc caagtccttg aactcagcag aaatagacca 1450
 tgtgaaaact ccattgcttg ttagcatctc caactccta tgtaaatcaa 1500
 caactgcat aataaataaa aggcaatcat gttata 1536

0010 • 358
 0011 • 273
 0012 • PRT
 0013 • Homo sapiens

0400 • 358
 Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu
 1 5 10 15
 Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser
 20 25 30
 Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp
 35 40 45
 Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val
 50 55 60
 Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu
 65 70 75
 His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser
 80 85 90
 Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr
 95 100 105
 Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu
 110 115 120
 Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe
 125 130 135
 Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val
 140 145 150
 Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu
 155 160 165

Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His		
	170	180
Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe		
	185	195
Ile Leu Val Asp Ser Gly Met Lys Glu Asn Gly Lys Val Ile Ser		
	200	210
Phe Phe Lys Leu Lys Glu Ser Gln Leu Pro Ala Leu Ala Ile Tyr		
	215	225
Gln Thr Leu Asp Asp Glu Trp Asp Thr Leu Pro Thr Ala Glu Val		
	230	240
Ser Val Glu His Val Gln Asn Phe Cys Asp Gly Phe Leu Ser Gly		
	245	255
Lys Leu Leu Lys Gln Asn Arg Glu Ser Glu Gly Lys Thr Pro Lys		
	260	270

Val Glu Leu

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<400> 359

ccagcagttgc ccatactcca tagr 24

<210> 360

<211> 20

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<400> 360

tgacgagtggt gatacactgc 20

<210> 361

<211> 24

<212> DNA

<213> Artificial Sequence

<210>

<213> Synthetic oligonucleotide probe

<400> 361

gctctacgga aacttttgtt gtgg 24

(C10): 362
 (C11): 50
 (C12): DNA
 (C13): Artificial Sequence

(C20):
 (C21): Synthetic oligonucleotide probe

(C40): 362
 attcccaagc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

(C10): 363
 (C11): 1777
 (C12): DNA
 (C13): Homo sapiens

(C40): 363
 ggagagagcgg ggctgggacc ggagtgggga gggggggctg gaggtgacac 50
 ccggcccggg tggcggagag atcagaagcc tcttccccaa gccgagccaa 100
 cctcaagcgg gaccggggct cagggacggg gggggggggg cggcgactgc 150
 agtggcttga cgatggcagg gtccggcgga gccggggggg tgattgcagg 200
 cccagcagc cggcgctggc tgtggtcggg gctggggggg ggccttgggc 250
 ccttgacagg tggagtatca gccttggaag tatataccc aaaagaaatc 300
 ttctgtttaa atggtacaca aggggaagctg acctgcaagt tcaagtctac 350
 tagtaagact ggggggttga cctcagtttc ctggagcttc cagccagagg 400
 gggccgacac tactgtgtcg ttttccact acctcccaagg gcaagtgtac 450
 cttgggaatt atccaccatt taaagacaga atcagcttgg ctggagacct 500
 tgacaagaaa gatgcattca tcaacataga aaatatgcag tttatacaca 550
 atggcactta tatctgtgat gtcaaaaaac ctctgacat cgttgtccag 600
 cctggacaca ttaggcctta tgtcgtagaa aaagagaatt tgcctgtgtt 650
 tccagtttgg gtagtgggtg gcatagttac tgcctgtgtc ctaggctctc 700
 ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750
 aaacgggatt acaactggctg cagtaacatc gagagtttgt caccagttaa 800
 gcaggctcct cggaaagtccc cctccgacac tgagggtctt gtaaagagtc 850
 tgctttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900
 tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
 tgccgatata cgaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtage ccattaccac 1050
 atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100
 ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcac 1150
 cctgatatga ggagccagt ttgcctgatg aaaagatggg atgattctac 1200
 atatgtacc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 caattgggag atttcagaaa ccttccttcc accatcattt agaaatgggt 1300
 tgccttaatg gagacaatag cagatccctg agtatttcca gtagacatgg 1350
 ccttttaata taagggttta agactgatta gtcttagcat ttaactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450
 cagtatcagt accatttatt tgtctgcgcg ttttaaaaaa taaccattgg 1500
 ctatgcacat tgaataaat ttgagaagtt tttttgaagt tttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttaactttaag 1600
 ttgcacccct tgaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaag gataaatgac gaaggtaact tcattctgga cacagttgga 1700
 tcaataactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtata ggtttta 1777

0210 - 364
 0211 - 269
 0212 - PET
 0213 - Homo sapiens

0400 - 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90

Ser	Gln	Gly	Gln	Val	Tyr	Leu	Gly	Asn	Tyr	Pro	Pro	Phe	Lys	Asp	95	100	105
Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile	110	115	120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys	125	130	135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile	140	145	150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val	155	160	165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr	170	175	180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn	185	190	195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser	200	205	210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly	215	220	225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile	230	235	240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile	245	250	255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn		260	265	

<210> 365

<211> 1321

<212> DNA

<213> Homo sapiens

<400> 365

gagggtgtgtg cagagaagcc atgtaccggc tctgttcagg agtgaactgcc 50

gggggtgagg ccccccgggg cttgggctca agctgaggac gacggggggg 100

ccatcagagg gcccgggtgc cgcctctcgg ccacgggttg gtccgggggc 150

tgggggtggg gctgggggtg gcgtccgggg tgaagtggg aggtggggctg 200

aggggggggg ccccccggca gtccccggcg gcccgcgacc ctgaggcgctc 250

gcctctggcc gagccgcacc aggagcagtc cctcgccccc tgggtctccgc 300

agaccccggc ggcgcctctg tccaggtgct tcgcacagag catcgagagg 350

agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcac 400

agtgggttggga gttttctgtag atggaaaaga agtctgggtca gaagggttag 450
 gttatgctga tgttgagaac cgtgtaacct gtaaacaga gacagttatg 500
 cgaattgcta gcatcagcaa aagtctcacc atgggttgctc ttgcccatt 550
 gtgggaagca gggaaaactgg atcttgatat tccagtacaa cattatgttc 600
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgcacacaa 650
 agattactga tttccatttt aagtgggaatt cgtcattatg aaaaggacat 700
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agaatgtttg atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gattttacta aatttaaaac agagcaggag aatgaagcaa aatgocggaa 850
 ttcaaaacct ggcaagaaaa agaattgatt tgaacaaggc gaattatatt 900
 tgagagaaaa gtttgaaaat tcaattgaat cctaagatt atttaaaaat 950
 gatcctttgt tcttcaaac tgytagtcag ttcttgatatt caacttttgg 1000
 ctataccta ctggcagcaa tagtagagag agcttcagga tgtaaatatt 1050
 tggactatat gcagaaaata ttccatgact tggatatgtt gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggc aaatgaatac 1150
 cttctgtgtg gtctagctat atgcctctt aacactattt tattaattaa 1200
 aagtcacatt ttctttgttt ccattccaaa atcaacctgc cacatttttg 1250
 gagcttttct acatgtctgt ttctcctct gtaaagtgaa ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met	Tyr	Arg	Leu	Leu	Ser	Ala	Val	Thr	Ala	Arg	Ala	Ala	Ala	Pro
1				5				10						15
Gly	Gly	Leu	Ala	Ser	Ser	Cys	Gly	Arg	Arg	Gly	Val	His	Gln	Arg
				20				25						30
Ala	Gly	Leu	Pro	Pro	Leu	Gly	His	Gly	Trp	Val	Gly	Gly	Leu	Gly
				35				40						45
Leu	Gly	Leu	Gly	Leu	Ala	Leu	Gly	Val	Lys	Leu	Ala	Gly	Gly	Leu
				50				55						60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu	65	70	75
Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro	80	85	90
Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100	105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115	120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130	135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145	150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160	165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175	180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190	195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205	210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220	225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235	240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250	255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265	270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280	285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295	300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310	315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325	330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340	345

Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val
 350 355 360

Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg
 365 370

<210> 367

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 367

ttggaagaa gtctggtcag aaggtttagg 30

<210> 368

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

tttttggtt cattctctg ctctg 25

<210> 369

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 369

aaaacctcag aacaactcat ttgcacc 28

<210> 370

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 370

gtctaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371

<211> 1150

<212> DNA

<213> Homo sapiens

<400> 371

gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcggct cgaggetggt gggaagaagc cgagatggcg gcagccagcg 100
 ctggggcacaac ccggetgctc ctgctcttgc tgatggcggt agcagcgccc 150
 agtcgagccc ggggcagcgg ctgcggggcc gggactggcg ccgagggggc 200
 tggggcggaa ggtcagagag ggagggcctg tggcacggcg gggctgctgc 250
 tggagcactc atttgagatc gatgacagtg ccaacttcgg gaagcggggc 300
 tcactgctct ggaaccagca ggatggtaac ttgtccctgt cacagcggca 350
 gctcagcgag gaggagcggg gcgactccg ggatgtggca gccctgaatg 400
 gctgttaccg ggtccggatc ccaagcgac ccggggccct ggatggcctg 450
 gaagctggcg gctatgtctc ctcttttgc cctggctgt cctgggtgga 500
 gtgcacctg tgggaccagc tgacctgca cgtggatgtg gccggcaacg 550
 tggcggcggt gtgggtggcg acccaccacg gggctgcgc gggccatgag 600
 gtggaggagc tggacctgga gctgttcaac acctcggctg agctgcagcc 650
 gccaccaca gccccaggcc ctgagacggc ggccttcatt gagcgccctg 700
 agatggaaca ggcacagaag gcccaagaac cccaggagca gaagtccctc 750
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 gtcaggagca ccagacaccg ggggcacggg tggggcggg ggtgggggtg 850
 gtggtggggg tagtggcctt tgtgtgtgc caccctccct gtaagtctat 900
 ttaaaacat cgaagataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcacag agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaattc actgctcact tgatactta ttcagaaaac 1050
 caagggaatgg ctgtcccat cctcctgtgg ctgtgtggag ctcagctgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15

Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30

Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu	35	40	45
Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<110> 373

<111> 1706

<112> DNA

<113> Homo sapiens

<400> 373

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gcctggcgcc ctggagccgg acgtgtccgg ggctccccc cagacccggg 100

cagcaggtcg tcggggggcc caccatgctg gtgaactgctt aacttgcttt 150
 tgtaggcctc ctggcctcct ggcctggggtt ggaactgtca agatgcgggg 200
 ctaaaacccc tgggaaggcc tgcagcaatc cctccttctt tgggtttcaa 250
 ctgggaattct atcaggtcta cttcctggcc ctggcagctg attggttca 300
 ggccccctac ctctataaac tctaccagca ttactacttc ctggaaggtc 350
 aaattgcat cctctatgtc tgtggccttg cctctacagt cctctttggc 400
 ctagtggcct cctccttgtt ggattggctg ggtcgcaaga attcttctgt 450
 cctctttctc ctgaacttact cactatgttg ctttaacaaa ctctctcaag 500
 actactttgt gctgctagtg gggcgagcac ttggtgggct gtccacagcc 550
 ctctcttctt cagccttcca ggcttggtat atccatgagc acgtggaaag 600
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 ctctggaaca tctgctggct gtatggcag gctggcagc tgaggctgta 700
 ggcagctgga tagggctggg gctgtagcg ccttttcttg ctgcacccc 750
 tctcctggct ctggcagggg ccttggcctt tggaaacttg ggggagaaat 800
 atgacgggca gctgctcttc tcaaggacct gtctgggagg cctgccttgc 850
 ctctgtctgg accgcgggtt gctgctgctg ggcacacac aagctctatt 900
 tgagagtgtc atcttcctct ttgtcttctt ctggacacct gtctgggacc 950
 cacacggggc cctctggggt attatctctt ccagcttcat ggcagccagc 1000
 ctgcttggct cttcctctga cgttatcgcc acctccaaga ggtaacacct 1050
 tcaagccatg cactgctgtt ccttgcctgt gctcctcttc gtctctcttc 1100
 tcttcctgtt gactttctct accagcccag ggcaggagag tcgggtggag 1150
 tcttcctatg cctttctact tattgagttg gcttctggat tatacttct 1200
 cagcatgagc ttctacgga gaaaggctat cctgagaca gagcaggctg 1250
 gtgtactcaa ctggttcagg gtactcttc actcactggc ttgcctaggg 1300
 ctctctgtcc tccatgacag tgatcgaaaa acaggcactc ggaatatggt 1350
 cagcatttgc tctgctgtca tggctgatgg tctgctggca gtggtgggac 1400
 tcttcacctt ggttaaggcat gatgctgagc tggggctacc ttcacctact 1450
 gaggagcctt atgcctctga gctgtaaccc cactccagga caagatagct 1500

gggacagact cttgaattcc agctatccgg gattgtacag atctctctgt 1550
 gactgaattt gtgactgtcc tgtgggtttct cctgccattg ctttgtgttt 1600
 gggaggacat gatgggggtg atggactgga aagaaggtag caaaagtcc 1650
 ctctgtgtta ctccattta gaaaataaac acttttaaat gatcaaaaaa 1700
 aaaaaa 1706

(210) 374
 (211) 450
 (212) PET
 (213) Homo sapiens

(400) 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15
Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20				25						30
Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35				40						45
Pyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50				55						60
Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65				70						75
Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80				85						90
Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95				100						105
Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110				115						115
Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125				130						135
Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140				145						150
Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155				160						165
Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170				175						180
Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185				190						195
Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200				205						210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn	
				215					220					225	
Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu	
				230					235					240	
Arg	Cys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	
				245					250					255	
Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	
				260					265					270	
Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	
				275					280					285	
Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	
				290					295					300	
Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	
				305					310					315	
Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	
				320					325					330	
Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	
				335					340					345	
Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	
				350					355					360	
Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	
				365					370					375	
Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	
				380					385					390	
Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	
				395					400					405	
Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	
				410					415					420	
Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	
				425					430					435	
Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	
				440					445					450	

(210) 375

(211) 1093

(212) DNA

(213) Homo sapiens

(400) 375

gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccggggcccg 50

gccctggaga tggccccgg cgcgcggggc tgggtgttgtc tegtgtctctg 100
 gctccccggg tgcgtcgggg cccacggcctt ccgtatccat gattatttgt 150
 accttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
 ccgtgccaagg accttggttg tatctttcac acaaggatatg agcagattca 250
 cctgtccccc gctgaacctc cagaggcctg cgggggaactc agcaacgggt 300
 ccttcaccca ggaccagatt gctctgttggt agaggggggg ctgctccttc 350
 ctctccaaga ctgggttggt ccaggagcac gggggggggg cggtgatcat 400
 ctctgacaac gcagttgaca atgacagctt ctactggag atgatccagg 450
 acagtaacca ggcacagct gacatccccg cctcttctct gctcggccga 500
 gacggctaca tgatccggcg ctctctggaa cagcatgggc tgccatgggc 550
 catcatttcc atccagtca atgtcaccag catcccccac tttgagctgc 600
 tgcacccggc ctggaacctc tggtagaaga gtttgtccca cattccagcc 650
 ataagtgaat ctgagctggg aaggggaaaac ccaggaattt tgcacttgg 700
 natttgagga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750
 tttggggggt gctaggtga aagggaagcc acaccactgg ccttcccttc 800
 cccagggccc ccaagggtgt ctcatgctac aagaagaggg aagagacagg 850
 cccaggggt tctgggtaga acccgaaaca aaaggagctg aaggcaggtg 900
 gctgagagg catctgtgac ctgtcacact cactgggtc cagcctccc 950
 taccaggggt ctctgcacag tgaccttcac agcagttgtt ggagtggttt 1000
 aaagagctgg tgtttgggga ctcaataaac cctcactgac ttttagcaa 1050
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5				10						15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20					25						30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35					40						45

Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr	50	55	60
Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly	65	70	75
Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val	80	85	90
Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln	95	100	105
Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp	110	115	120
Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg	125	130	135
Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr	140	145	150
Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile	155	160	165
Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu	170	175	180
Leu Gln Pro Pro Trp Thr Phe Trp	185		

00100 377

00110 496

00120 DNA

00130 Homo sapiens

00200

00210 unsure

00220 396

00230 unknown base

04000 377

tctgcctcca ctgctctgtg ctgggacat ggaacttgca ctgctgtgtg 50

ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100

ctgaacaaga tggccaagca agtgactggg aaaatgccca tctctocta 150

ctggcctac ggctgtcact gggactagg tggcagaggc caacccaaag 200

atgccaaggga ctggtgtgtc cagaccatg actgtgtgta tgaccacctg 250

aagaccagg ggtgoggcat ctacaaggac aacaacaaaa gcagcataca 300

ttgtatggat ttatctcaac gctattgttt aatgggtgtg tttaatgtga 350

tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 495

<210> 378

<211> 116

<212> PPT

<213> Homo sapiens

<400> 378

Met Glu Leu Ala Leu Leu Cys Gly Leu Val Val Met Ala Gly Val
1 5 10 15

Ile Pro Ile Gln Gly Gly Ile Leu Asn Leu Asn Lys Met Val Lys
20 25 30

Gln Val Thr Gly Lys Met Pro Ile Leu Ser Tyr Trp Pro Tyr Gly
35 40 45

Cys His Cys Gly Leu Gly Gly Arg Gly Gln Pro Lys Asp Ala Thr
50 55 60

Asp Trp Cys Cys Gln Thr His Asp Cys Cys Tyr Asp His Leu Lys
65 70 75

Thr Gln Gly Cys Gly Ile Tyr Lys Asp Asn Asn Lys Ser Ser Ile
80 85 90

His Cys Met Asp Leu Ser Gln Arg Tyr Cys Leu Met Ala Val Phe
95 100 105

Asn Val Ile Tyr Leu Glu Asn Glu Asp Ser Glu
110 115

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 379

ctgacctccac tgctctgtgc tggg 24

<210> 380

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

caagagcagtg gatgttcccc tggg 24

<210> 381

<211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Synthetic oligonucleotide probe

<400> 381
 ctgaacaaga tggtaagca agtgactggg aaaatgccca tcttc 45

<210> 382
 <211> 764
 <212> DNA
 <213> Homo sapiens

<400> 382
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 gggcatgttg aggggtgccc gcaacaaccag acgcccagtc acaggcgaga 100
 gctctgggat gcaacggcca gaggccatgc tgcctgtgtc caagcttgc 150
 ctctctgggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200
 caagtatttc agcaccctg aagactaaga ccattgaaatc acagggctgc 250
 ggtgtctgt aggtctcttc ctggtgaaaa gtgtccaggt gaaaattgga 300
 gactctggg acgtgaaact gggagctta ggtgggaata cccaggaagt 350
 caacctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400
 ctctctccg gggatgttc atgtacacca gcaaggacg ctattcttat 450
 ttggggaagc ttgatggca gatctctct gctaccaca gccaagaggg 500
 gagggtgtg gtgggcctct atggccagta tcaactcctt ggcattcaaga 550
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 ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650
 ggtatggggc catccagct gaggccatct gtgtggtggt ggtgatggt 700
 actggagtaa ctgagtggg acgtgaatc tgaatccacc aataaataaa 750
 gcttctgcag aaaa 764

<210> 383
 <211> 173
 <212> PRT
 <213> Homo sapiens

<400> 383
 Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
 1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
 20 35 50
 Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
 35 50 65
 Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln
 50 65 80
 Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly
 65 80 95
 Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr
 80 95 110
 Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met
 95 110 125
 Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly
 110 125 140
 Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val
 125 140 155
 Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly
 140 155 170
 Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro
 155 170 185
 Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg
 170 185

<210> 314
 <211> 2179
 <212> DNA
 <213> Homo sapiens

<400> 314
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 agctctgtgg ctgaactggg tgcctcatcac gggaactgct gggctatgga 100
 atacagatgt ggcagctcag gtagccccaa attgcctgga agaatacatc 150
 atgtttttcg atangaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccacaa aaactgtaaa gatgcacaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgcg ggaatgcgg 300
 tgttggtgatt tatgtgtctc tggagtgttc tgcgtggctg gcaaagaata 350
 atgttccaaa atcgttcacat ccccaagggt gtcacatttt ttttctcggg 400
 tgtcagcgag cctgactca ctacagtcca gctgacaggg gctgtcatgc 450

aactggcccc taagccaaaag caaaagacct aaggacgacc tttgaacaat 500
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(210) 335
 (211) 513
 (212) PRT
 (213) Homo sapiens

(400) 385
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 35 40 45
 Tyr Cys Glu Ser Gln Lys Leu Gln Glu Ile Pro Ser Ser Ile Ser
 50 55 60
 Ala Gly Cys Leu Gly Leu Ser Leu Arg Tyr Asn Ser Leu Gln Lys
 65 70 75
 Leu Lys Tyr Asn Gln Phe Lys Gly Leu Asn Gln Leu Thr Trp Leu
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 Tyr Leu Asp His Asn His Ile Ser Asn Ile Asp Glu Asn Ala Phe
 95 100 105
 Asn Gly Ile Arg Arg Leu Lys Glu Leu Ile Leu Ser Ser Asn Arg
 110 115 120
 Ile Ser Tyr Phe Leu Asn Asn Thr Phe Arg Pro Val Thr Asn Leu
 125 130 135
 Arg Asn Leu Asp Leu Ser Tyr Asn Gln Leu His Ser Leu Gly Ser
 140 145 150

Glu Gln Phe Arg Gly Leu Arg Lys Leu Leu Ser Leu His Leu Arg	155	160	165
Ser Asn Ser Leu Arg Thr Ile Pro Val Arg Ile Phe Gln Asp Cys	170	175	180
Arg Asn Leu Glu Leu Leu Asp Leu Gly Tyr Asn Arg Ile Arg Ser	185	190	195
Leu Ala Arg Asn Val Phe Ala Gly Met Ile Arg Leu Lys Glu Leu	200	205	210
His Leu Glu His Asn Gln Phe Ser Lys Leu Asn Leu Ala Leu Phe	215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr Leu Gln Trp Asn Lys	230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser Trp Thr Trp Ser Ser Leu	245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu Ile Glu Ala Phe Ser Gly	260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn Leu Gln Arg Leu Asn Leu	275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly Gln Glu Ile Leu Asp Ser	290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu Ala Gly Asn Ile Trp Glu	305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val Asn Trp Leu Lys Ser Phe	320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile Cys Ala Ser Pro Lys Glu	335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala Val Lys Asn Tyr Ser Ile	350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe Asp Leu Ala Arg Ala Leu	365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu Pro Arg Pro Lys His Glu	380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val Gly Ala Thr Glu Pro Gly	395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His Ile Ser Phe His Lys Ile	410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu Ser Val Leu Val Ile Leu	425	430	435

Leu Val Ile Tyr Val Ser Trp Lys Arg Tyr Pro Ala Ser Met Lys
 440 445 450

Gln Leu Gln Gln Arg Ser Leu Met Arg Arg His Arg Lys Lys Lys
 455 460 465

Arg Gln Ser Leu Lys Gln Met Thr Pro Ser Thr Gln Glu Phe Tyr
 470 475 480

Val Asp Tyr Lys Pro Thr Asn Thr Glu Thr Ser Glu Met Leu Leu
 485 490 495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
 500 505 510

Cys Glu Val

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 386

ctgggatctg aacagtttcg gggc 24

<210> 387

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 387

gggtccacagg acatggtctg tccc 24

<210> 388

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 388

gctgagatta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 389

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 ctoggaccta ccattgogaag aagatgaaat gtgtgtaaat tataatgacc 200
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<210> 390
 <211> 146
 <212> PPT
 <213> Homo sapiens

<400> 390
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 20 25 30
 Leu Pro Cys Glu Glu Asp Glu Met Cys Val Asn Tyr Asn Asp Gln
 35 40 45
 His Pro Asn Gly Trp Tyr Ile Trp Ile Leu Leu Leu Val Leu
 50 55 60
 Val Ala Ala Leu Leu Cys Gly Ala Val Val Leu Cys Leu Gln Cys
 65 70 75
 Trp Leu Arg Arg Pro Arg Ile Asp Ser His Arg Arg Thr Met Ala
 80 85 90
 Val Phe Ala Val Gly Asp Leu Asp Ser Ile Tyr Gly Thr Glu Ala
 95 100 105
 Ala Val Ser Pro Thr Val Gly Ile His Leu Gln Thr Gln Thr Pro
 110 115 120
 Asp Leu Tyr Pro Val Pro Ala Pro Cys Phe Gly Pro Leu Gly Ser
 125 130 135
 Pro Pro Pro Tyr Glu Glu Ile Val Lys Thr Thr
 140 145

<210> 391
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 391
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<210> 392
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 293

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 343

ccagtttggtg ctctcggacc taccatgca agaagatgaa atgtgtg 47

<210> 334

<211> 2340

<212> DNA

<213> Homo sapiens

<400> 334

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gagcagctg acccccgtt attagctctc gctgcgtcgc ccgggtccag 150
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<210> 395

<211> 140
 <212> PRT
 <213> Homo sapiens

<400> 396

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				20				25					30	
His	Tyr	Thr	Phe	Gln	Gln	Pro	Arg	His	Gln	Ser	Ser	Val	Lys	Leu
				35				40					45	
Arg	Glu	Gln	Ile	Leu	Asp	Leu	Ser	Lys	Arg	Tyr	Val	Lys	Ala	Leu
				50				55					60	
Ala	Glu	Glu	Asn	Lys	Asn	Thr	Val	Asp	Val	Glu	Asn	Gly	Ala	Ser
				65				70					75	
Met	Ala	Gly	Tyr	Ala	Asp	Leu	Lys	Arg	Thr	Ile	Ala	Val	Leu	Leu
				80				85					90	
Asp	Asp	Ile	Leu	Gln	Arg	Leu	Val	Lys	Leu	Glu	Asn	Lys	Val	Asp
				95				100					105	
Tyr	Ile	Val	Val	Asn	Gly	Ser	Ala	Ala	Asn	Thr	Thr	Asn	Gly	Thr
				110				115					120	
Ser	Gly	Asn	Leu	Val	Pro	Val	Thr	Thr	Asn	Lys	Arg	Thr	Asn	Val
				125				130					135	
Ser	Gly	Ser	Ile	Arg										
				140										

<210> 396
 <211> 1639
 <212> DNA
 <213> Homo sapiens

<400> 396

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<010> 397

<011> 353

<012> PET

<013> Homo sapiens

<000> 397

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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu	Thr
				20					25					30

Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys	Ser
				35					40					45

Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp	Thr
				50					55					60

Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn	Glu
				65					70					75

Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu	Asp
				80					85					90

Leu Ser His Asn	Leu Leu Thr Ser Ile	Ser Pro Thr Ala Phe Ser
95	100	105
Arg Leu Arg Tyr	Leu Glu Ser Leu Asp	Leu Ser His Asn Gly Leu
110	115	120
Thr Ala Leu Pro	Ala Glu Ser Phe Thr	Ser Ser Pro Leu Ser Asp
125	130	135
Val Asn Leu Ser	His Asn Gln Leu Arg	Glu Val Ser Val Ser Ala
140	145	150
Phe Thr Thr His	Ser Gln Gly Arg Ala	Leu His Val Asp Leu Ser
155	160	165
His Asn Leu Ile	His Arg Leu Val Pro	His Pro Thr Arg Ala Gly
170	175	180
Leu Pro Ala Pro	Thr Ile Gln Ser Leu	Asn Leu Ala Trp Asn Arg
185	190	195
Leu His Ala Val	Pro Asn Leu Arg Asp	Leu Pro Leu Arg Tyr Leu
200	205	210
Ser Leu Asp Gly	Asn Pro Leu Ala Val	Ile Gly Pro Gly Ala Phe
215	220	225
Ala Gly Leu Gly	Gly Leu Thr His Leu	Ser Leu Ala Ser Leu Gln
230	235	240
Arg Leu Pro Glu	Leu Ala Pro Ser Gly	Phe Arg Glu Leu Pro Gly
245	250	255
Leu Gln Val Leu	Asp Leu Ser Gly Asn	Pro Lys Leu Asn Trp Ala
260	265	270
Gly Ala Glu Val	Phe Ser Gly Leu Ser	Ser Leu Gln Glu Leu Asp
275	280	285
Leu Ser Gly Thr	Asn Leu Val Pro Leu	Pro Glu Ala Leu Leu Leu
290	295	300
His Leu Pro Ala	Leu Gln Ser Val Ser	Val Gly Gln Asp Val Arg
305	310	315
Cys Arg Arg Leu	Val Arg Glu Gly Thr	Tyr Pro Arg Arg Pro Gly
320	325	330
Ser Ser Pro Lys	Val Pro Leu His Cys	Val Asp Thr Arg Glu Ser
335	340	345
Ala Ala Arg Gly	Pro Thr Ile Leu	
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<C10> 398

<C11> 23

<C12> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

cactggccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

gggttggtgcc cgaaaggctc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

caaacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gatgggcacg ccacagcttc tgtgagattc gattttctcc cagttccct 50

gtgggtctga ggggaccaga agggtagact acgttggtt totggaaggg 100

gaggctatat ggcacaattc cccaaaacaa gttttgacat ttcccttgaa 150

atctcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgaggc ctaacggggg agccaggatg gggacagaat aaaggagcca 250

cgactcttgc caccactcg cactcagaact ctgaactcag acctgaaatc 300

ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350

ttccagacct aagatgaaaag cctctagtct tgccttcagc cttctctctg 400

ctggttttta tctctatggt actccttcca ctggactgaa gacaotcaat 450

ttgggaagct gtgtgatcgc cacaacctt caggaaatac gaaatggatt 500

ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550

gaatcttaag gaggaactgag tctttgcaag acacaaagcc tgcgaatoga 600
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 gggaactaga cattctttct caatggatgg aggagacaga ataggaggaa 900
 agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950
 acctgcagag gaggcctgac cccaaaaccac catctcttta ctgtactagt 1000
 cttgtgctgg tccagtgta tottatttat gcattacttg ctctcttga 1050
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 attttctaa tatctttctg ctattggata tatttattag ttaatatatt 1150
 tatttatttt ttgctattta atgtatttat ttttttactt ggacatgaaa 1200
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 gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400
 tctggaataa gttttgatgt ggaattgcac acctacctta caattactga 1450
 ccacccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500
 aatccacac gccacgcatg tatttctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402
 <211> 261
 <212> PRT
 <213> Homo sapiens

<400> 402
 Met Arg Gln Phe Pro Lys Thr Ser Phe Asp Ile Ser Pro Glu Met
 1 5 10 15
 Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu
 20 25 30
 Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys
 35 40 45

Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu	50	55	60
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu	65	70	75
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser	80	85	90
Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

(210) 403

(211) 28

(212) DNA

(213) Artificial Sequence

(220)

(225) Synthetic oligonucleotide probe

(400) 403

ctctctgtggt ctccagattt caggccta 28

(210) 404
 (211) 26
 (212) DNA
 (213) Artificial Sequence

(220)
 (225) Synthetic oligonucleotide probe

(400) 404
 agtctctctt aagattctga tgtcaa 26

(210) 405
 (211) 238
 (212) DNA
 (213) Homo sapiens

(400) 405
 ccgttatcgt cttgcgctac tgcgtgaatgt ccgtcccgga ggaggaggag 50
 aggtctttgc cgcctgaccca gagatggccc cgagcgagca aattcctact 100
 gtccgggtgc ggggctaccc tgcgcgagct agcaaccttt cccctggatc 150
 ccacaaacac ccgactccaa atgcaaggag aagcagctct tgcctgggtg 200
 ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
 cctagggtac attgaagagg aaggtcttct aaagctttgg caaggagtga 300
 caccggccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350
 tatgaacatc ccgagagggt tctgttttgg aaaagtgaag atgagcatta 400
 tcccccttgg aaatcagtca ctggagggat gatggctggg gttattggcc 450
 agttttttag caatccaaat gacctagtga aggttcagat gcaaatggaa 500
 ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550
 tgcatttgca aaaatcttag ctgaaggagg aatacagggg ctttgggcag 600
 gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650
 accacttatg atacagtga aactacttgg gtattgaata caccacttga 700
 ggacaatata atgactcacg gtttatcaag tttatgttct ggactggtag 750
 cttctattct gggaaacacca gcgatgtca tcaaaagcag aataatgaat 800
 caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
 ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
 gctttttacc atcttgggtg agaatgaccc cttggccaat ggtgttctgg 950
 cttacttatg aaaaaatcag agagatgagt ggagtcagtc catttttaa 998

<C110> 406
 <C111> 323
 <C112> PFT
 <C113> Homo sapiens

<C400> 406

Met	Ser	Val	Pro	Glu	Glu	Glu	Glu	Arg	Leu	Leu	Pro	Leu	Thr	Gln
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Arg	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala
				20					25					30
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr
				35					40					45
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp
				50					55					60
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala
				65					70					75
Leu	Gly	Ile	Ile	Gln	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly
				80					85					90
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg
				95					100					105
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser
				110					115					120
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met
				125					130					135
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu
				140					145					150
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly
				155					160					165
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile
				170					175					180
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro
				185					190					195
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr
				200					205					210
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu
				215					220					225
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu
				230					235					240
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg
				245					250					255

Ile Met Asn Gln Pro Arg Asp Lys Gln Gly Arg Gly Leu Leu Tyr	
	260 265 270
Lys Ser Ser Thr Asp Cys Leu Ile Gln Ala Val Gln Gly Glu Gly	
	275 280 285
Phe Met Ser Leu Tyr Lys Gly Phe Leu Pro Ser Trp Leu Arg Met	
	290 295 300
Thr Pro Trp Ser Met Val Phe Trp Leu Thr Tyr Glu Lys Ile Arg	
	305 310 315
Glu Met Ser Gly Val Ser Pro Phe	
	320

(210) 407

(211) 31

(212) DNA

(213) Artificial Sequence

(320)

(321) Synthetic oligonucleotide probe

(400) 407

gggggatccc gttatcgtct tgcgctaactg c 31

(210) 408

(211) 34

(212) DNA

(213) Artificial Sequence

(320)

(321) Synthetic oligonucleotide probe

(400) 408

ggggaattct taaaatggac tgactccact catc 34

(210) 409

(211) 1487

(212) DNA

(213) Homo sapiens

(400) 409

gggaagggtg ggagggggac gcgggcaggg ttgtggcgca gcagtctcct 50

tcctggcgcg gcgcctgaag tcggcggtggg cgtttjagga agctgggata 100

cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150

agataaattt tcgttggcca gaatgtgaat gtattgactg gattgagaga 200

agaaatgctg tggcatctgt tgtgcaggt atattgttt ttacaggctg 250

gttgataatg attgatgcag ctgtgggtgta tcttaagcca gaacagttga 300

accatgcctt tcacacatgt ggtgtatttt ccacattggc tttcttcatg 350

ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400
 ctgttttagga agaacagggtg ctcgagtttg gcttttccatt ggtttccatgt 450
 tgatgtttgg gtcacttatt gcttccatgt ggattctttt tgggtgcatt 500
 gttacccaaa ataactgatgt ttatccggga ctagctgtgt tttttcaaaa 550
 tgcacttata ttttttagca ctctgatcta caaatttggga agaaccgaag 600
 agctatggac ctgagatcac ttcttaagtc acattttctt ttgtttatat 650
 tctgtttgta gataggtttt ttctctctca gtacacattg ccaaatggag 700
 tagattgtac attaaatgtt ttgtttcttt acatttttat gttctgagtt 750
 ttgaaatagt tttatgaaat ttctttattt ttcattgcct agactgttaa 800
 tatgtatata atacaagact atatgaattg gataatgagt atcagttttt 850
 tattctgag atttagaact tgatctactc cctgagccag ggttacatca 900
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 gctcatgctt gtaatccag cacttttggga ggccgaggcg ggccgattgc 1000
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 taactaaaaat acaaaaatta gccaggcatg gtggtgggtg cctgtaatcc 1100
 cagctacttg ggaggctgag gcaggagaat cgtttgaacc cggggggcag 1150
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 cataaaaaggt tttcagcaag ttgtaactta ttttggccta aaaatgaggt 1350
 ttttttggtt aagaaaaaat atttgttctt atgtattgaa gaagtgtact 1400
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 ctaaaaagaa ttctctaat atgactttat gtgagaa 1487

<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25				30	

Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala	
				35					40					45	
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr	
				50					55					60	
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val	
				65					70					75	
Ser	Asn	Ala	Gln	Val	Arg	Gly	Asp	Ser	Tyr	Glu	Ser	Gly	Cys	Leu	
				80					85					90	
Gly	Arg	Thr	Gly	Ala	Arg	Val	Trp	Leu	Phe	Ile	Gly	Phe	Met	Leu	
				95					100					105	
Met	Phe	Gly	Ser	Leu	Ile	Ala	Ser	Met	Trp	Ile	Leu	Phe	Gly	Ala	
				110					115					120	
Tyr	Val	Thr	Gln	Asn	Thr	Asp	Val	Tyr	Pro	Gly	Leu	Ala	Val	Phe	
				125					130					135	
Phe	Gln	Asn	Ala	Leu	Ile	Phe	Phe	Ser	Thr	Leu	Ile	Tyr	Lys	Phe	
				140					145					150	
Gly	Arg	Thr	Glu	Glu	Leu	Trp	Thr								
				155											

<210> 411

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

tttgaggaa gctgggatac 20

<210> 412

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccaaactcga gcaactgttc 20

<210> 413

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

(1400) 413

atggcaggct tectagataa ttttcgttgg ccagaatgtg 40

(1210) 414

(1211) 1337

(1212) DNA

(1213) Homo sapiens

(1400) 414

gttgatggca aacttctcca aaggaggggc agagcctggc cagggcagga 50

gcagctgggc cactgggggc ccgcaaacct ccgtctcacc ctctggggcc 100

actgcctcta gaggaggggc gtctgtgagg ccactacccc tccagcaact 150

gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200

gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250

aagtgggagc ctgagccct cgggtggaag ctgaccccaa gccacccttc 300

acctggacag gatgagagtg tcaggtgtgc ttgacctctt ggccctcacc 350

tttgccatag tcaagacatg gatgtttatt cgaagctaca tgagcttcag 400

catgaaaaac atccgtctgc cactgtggct ggcagcctcg ccacccaagg 450

agatccaggt taaaaagtac aagtgtgggc tcacccaagg ctgcccagcc 500

aactactttg cgtttaaaat ctgcagtggg gcggccaaag tctgtggccc 550

tactatgtgc ttggaagacc gcctgacatc gactcctgtg aaaaacaatg 600

tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650

ctgggacaga aggcatttga catgtactct ggagatgtta tgcacctagt 700

gaaattcctt aaagaaattc cgggggggtgc actgggtgctg gtggccctct 750

acgacgctcc agggacccaa atgaacgatg aaagcaggaa actcttctct 800

gacttgggga gttctctacg aaaaacaactg ggcttccggg acagctgggt 850

cttccatagga gccaaaagacc tcaggggtaa aagccctttt ggcagttct 900

taaagaacag ccacagacaca aacaaatacg agggatgggc agagctgctg 950

gagatggagg gctgcctgcc ccggaagcca ttttaggggtg gctgtggctc 1000

ttctccagcc aggggcctga agaagctctt gcctgactta ggagtcagag 1050

ccgggcaggg gctgaggagg aggagcaggg ggtgctgggt ggaagggtgt 1100

gcaggtcctt gcaogctgtg tcgggcctct cctctctgga aacagaaacc 1150

tcccacagca cactctacc gccagaccag cctcagaggg tcttcttgga 1200

accagctgtc tgtggagaga atgggggtgt ttcgtcaggg actgctgacg 1250

gctgggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300

tatttttgct ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415

<211> 124

<212> PRT

<213> Homo sapiens

<400> 415

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Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser
20 25 30

Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr
35 40 45

Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro
50 55 60

Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala
65 70 75

Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met
80 85 90

Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu
95 100 105

Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp
110 115 120

Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu
125 130 135

Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro
140 145 150

Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu
155 160 165

Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val
170 175 180

Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln
185 190 195

Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro
200 205 210

Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe
215 220

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
ggcatagtca cgacatggat g 21

<210> 417
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggatggccag agctgctg 18

<210> 418
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
gaattcgaag tgtgacctca tcaagc 26

<210> 419
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
tcctgactcct aagtcaggca ggag 24

<210> 420
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 420
attctctcca cagacagctg gttc 24

<210> 421

(211) 46
 (212) DNA
 (213) Artificial Sequence

(220)
 (221) Synthetic oligonucleotide probe

(300) 471
 ggcacagcgt ggcccatca agccctgcc agccaactac ttgcgc 46

(210) 482
 (211) 1701
 (212) DNA
 (213) Homo sapiens

(220)
 (221) unsure
 (222) 1528
 (223) unknown base

(300) 412
 gagactccag agggagataa agagagaggg caaagaggca gcaagagatt 50
 tctctcggg atccagaaac ccattgatac ctactgaaca ccgaatcccc 100
 tggagccca cagagacaga gacagcaaga gaagcagaga taaatacaact 150
 cagcccagg gctcctctgc tetctctctc tetctctcac tctctctccc 200
 ctctctctc gctctctcta gctctctagt cctcaaatc ccagtcccc 250
 ggaaccta ctgggacact atgttgttct ccgcctctct gctggaggtg 300
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cgtacaaatg gctcgtctcac aactccccct tctaccaga gtgtgtcttg 950
 gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000
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 cagaactacc gagcccttca gctctcctaat cagcgcctgg tctttgcttc 1100
 tttcctccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150
 gtgttaggaat cttggttggc tgtctctgac tctctctggc tgtttatttc 1200
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 cttcactca gcacaagcca cgaactgaggc ataacttctt tctcagatac 1300
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 gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600
 tttcctaga tatactggcg gatctctctt taggataaag agttgctgtt 1650
 gaattgtat atttttgatc aatatatttg gaaactaaag tttctgactt 1700

- 1 01

(210) - 423
 (211) - 337
 (212) - PRT
 (213) - Homo sapiens

(400) - 423
 Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala
 1 5 10 15
 Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln
 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu
 80 85 90

Pro Ser Thr Leu Tyr Leu Gly Gly Leu	Pro Arg Lys Tyr Val Ala	
95	100	105
Ala Gln Leu His Leu His Trp Gly Gln	Lys Gly Ser Pro Gly Gly	
110	115	120
Ser Glu His Gln Ile Asn Ser Glu Ala Thr	Phe Ala Glu Leu His	
135	130	135
Ile Val His Tyr Asp Ser Asp Ser Tyr Asp	Ser Leu Ser Glu Ala	
140	145	150
Ala Glu Arg Pro Gln Gly Leu Ala Val	Leu Gly Ile Leu Ile Glu	
155	160	165
Val Gly Glu Thr Lys Asn Ile Ala Tyr Glu	His Ile Leu Ser His	
170	175	180
Leu His Glu Val Arg His Lys Asp Gln	Lys Thr Ser Val Pro Pro	
185	190	195
Phe Asn Leu Arg Glu Leu Leu Pro Lys Gln	Leu Gly Gln Tyr Phe	
200	205	210
Arg Tyr Asn Gly Ser Leu Thr Thr Pro	Pro Cys Tyr Gln Ser Val	
215	220	225
Leu Trp Thr Val Phe Tyr Arg Arg Ser Gln	Ile Ser Met Glu Gln	
230	235	240
Leu Glu Lys Leu Gln Gly Thr Leu Phe Ser	Thr Glu Glu Glu Phe	
245	250	255
Ser Lys Leu Leu Val Gln Asn Tyr Arg Ala	Leu Gln Pro Leu Asn	
260	265	270
Gln Arg Met Val Phe Ala Ser Phe Ile Gln	Ala Gly Ser Ser Tyr	
275	280	285
Thr Thr Gly Glu Met Leu Ser Leu Gly Val	Gly Ile Leu Val Gly	
290	295	300
Cys Leu Cys Leu Leu Leu Ala Val Tyr Phe	Ile Ala Arg Lys Ile	
305	310	315
Arg Lys Lys Arg Leu Glu Asn Arg Lys Ser	Val Val Phe Thr Ser	
320	325	330
Ala Gln Ala Thr Thr Glu Ala		
335		

<210> 424

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 414
gtaaagtcgc tggccagc 18

<210> 415
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 415
cccgatctgc ctgctgta 18

<210> 416
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 426
cttactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 427
cagaaaacca tgatacccta ctgaacaccg aatcccttg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
aatttttccac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50
acattttggcc tcttggaccc aaaggtagca atctgaaaca tgaggagtac 100
gattctactg ttttgtcttc taggatcaac tgggtcatta ccacagctca 150
aactgtgttt gggactccct ccacaaaaac tgggtccgga tcagggaaca 200
ctaccaaaac aacagcagtc aaatcaggtc tttccttctt taagtctgat 250
accattaaca cagatgctca cactgggggc agatctgcat ctgttaaata 300

ctgctgcagg aatgacacct ggtaccacaga cccacccatt gaccctggga 350
 ggggttgatg tacaacagca actgcaccca catgtgttac caatttttgt 400
 cacacaaactt ggagcccagg gaactatcct aagctcagag gaattgcac 450
 aaatcttcac gagctcctc atccattcct tgttcccggg aggcctcctg 500
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550
 agcaggagga gcagggtgaa atcctgcac ccaggggaac ccagcagggc 600
 gcttcaccaac tccagtggc acagatgag actttgcagt gaacacccct 650
 gcaggcatcc aaaggagcac acatgcctc gaggaagcca ccacagaatc 700
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgct 750
 cgaatttggt gatacatgtg aatctttatc attgattata ttatggaata 800
 gattgagaca cattggatag tcttagaaga aattaattct taatttaact 850
 caaaatattc ttgaaatttc agaaaatatg ttctatgtag agaataccaa 900
 ctttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950
 tatgtctgct ggatgatatg catattaaaa catatttgga aaactggaaa 1000
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050
 aaaaaaaaaa aaaaaaaaaa aaa 1073

(110): 429

(111): 209

(112): PRT

(113): Homo sapiens

(100): 429

Met	Arg	Ser	Thr	Ile	Leu	Leu	Phe	Cys	Leu	Leu	Gly	Ser	Thr	Arg
1				5					10					15
Ser	Leu	Pro	Gln	Leu	Lys	Pro	Ala	Leu	Gly	Leu	Pro	Pro	Thr	Lys
				20					25					30
Leu	Ala	Pro	Asp	Gln	Gly	Thr	Leu	Pro	Asn	Gln	Gln	Gln	Ser	Asn
				35					40					45
Gln	Val	Phe	Pro	Ser	Leu	Ser	Leu	Ile	Pro	Leu	Thr	Gln	Met	Leu
				50					55					60
Thr	Leu	Gly	Pro	Asp	Leu	His	Leu	Leu	Asn	Pro	Ala	Ala	Gly	Met
				65					70					75
Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr

	95	100	105
Gln Leu Gly Ala	Gln Gly Thr Ile Leu Ser Ser Glu Glu Leu Pro		
	110	115	120
Gln Ile Phe Thr Ser Leu Ile Ile His Ser Leu Phe Pro Gly Gly			
	125	130	135
Ile Leu Pro Thr Ser Gln Ala Gly Ala Asn Pro Asp Val Gln Asp			
	140	145	150
Gly Ser Leu Pro Ala Gly Gly Ala Gly Val Asn Pro Ala Thr Gln			
	155	160	165
Gly Thr Pro Ala Gly Arg Leu Pro Thr Pro Ser Gly Thr Asp Asp			
	170	175	180
Asp Phe Ala Val Thr Thr Pro Ala Gly Ile Gln Arg Ser Thr His			
	185	190	195
Ala Ile Glu Glu Ala Thr Thr Glu Ser Ala Asn Gly Ile Gln			
	200	205	

(210) 430
 (211) 1257
 (212) DNA
 (213) Homo Sapien

(400) 430
 ggagagagggc ggcggggtga aaggcgccatt gatgagccct ggcggggccct 50
 gggagcgagg cggagccaga cgtcgaccac gttccctccc tcgggtctct 100
 ccgctctccag ctccgggtgtg ccgggcagcc gggaagccatg ccgacccagg 150
 gccccggcgc ctcccccag cggctccggcg gctccctgct gctccctgctg 200
 ctgcagctgc ccggcgccgc gagcgctct gagatcccca aggggaagca 250
 aaaggcgcag ctccggccaga gggaggtggt ggaacctgtat aatggaatgt 300
 gcttacaagg gccagcagga gtgcttggtc gagaaggag ccctggggcc 350
 aatgtttatc cgggtacacc tgggaccca ggtcgggatg gattcaaagg 400
 agaaaagggg gaatgtctga gggaaagctt tgagggtcc tggacacca 450
 actacaagca gtgttcctgg agttcattga attatggcat agatcttggg 500
 aaaattggcg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
 agttttgttc agtggctcac ttgggtctaa atgcagaaat gcctgctgct 600
 agcgttggtg ttccacatc aatggagctg aatgttcagg acctcttccc 650
 attgaagcta taatttattt ggaccaagga agcctgaaa tgaattcaac 700

aattaatatt catogcaott cttctgtgga aggactttgt gaaggaattg 750
ctgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcacpattat 850
tgaagaacta ccaaaaataaa tgotttaatt ttcatttget acctottttt 900
ttattatgcc ttggaatggt tcaottaaat gacattttta ataatgttat 950
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200
aatttgtaaa tgttaagaat tttttttata tctgttaa at aaaaattatt 1250
tcaaca 1257

0210> 431
0211> 243
0212> PRT
0213> Hemo Sapien

0400> 431
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly
1 5 10 15
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala
20 25 30
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg
35 40 45
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala
50 55 60
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro
65 70 75
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys
80 85 90
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn
95 100 105
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu
110 115 120
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg
				140					145					150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu
				155					160					165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln
				170					175					180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser
				185					190					195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp
				200					205					210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp
				215					220					225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu
				230					235					240

Leu Pro Lys

<210> 432

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 432

aggacttgcc ctcaggaa 18

<210> 433

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 433

agcaggacag ttgtgaaaat a 21

<210> 434

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 434

atgacgctcg tccaaggcca c 21

<210> 435
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 4-5
ccacactgta ccaccatgt 19

<210> 436
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 4-6
acttcaggca ccactgttc tccc 24

<210> 437
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 4-7
caggc tggc attcaagtc 19

<210> 438
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
tgaactggca aaggaagaa 19

<210> 439
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 439
cagccacct ccagtcgaag g 21

<210> 440
<211> 19

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 440
 gggtcgtgtt ttggagaga 19

 <210> 441
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 441
 ctggcctca gacaccaat 20

 <210> 442
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 442
 tctctatca ctctcctag ctcca 25

 <210> 443
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 443
 ctggcaggag ttaaagttcc aaga 24

 <210> 444
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 444
 aaaggaccc gggatgtg 18

 <210> 445
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 445
agcgtagact ctctccaggc aaccag 26

<210> 446
<211> 22
<212> LNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 446
caattctgga tgaggtggta ga 12

<210> 447
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 447
cagactgag cgcttgctta 20

<210> 448
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 448
caaaaggcca agtaccggac c 21

<210> 449
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 449
ccagacstca gccaggaa 18

<210> 450
<211> 13
<212> DNA
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

ccctagetga ccccttca 18

<210> 451

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 451

tctyacaagc agttttctga atc 23

<210> 452

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 452

ctctccacct ccttttctct ttgttt 26

<210> 453

<211> 18

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 453

ctctggtgcc cacagtga 18

<210> 454

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 454

ccatgactgc tcagccaaga a 21

<210> 455

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 455
 cacgaaatct ggaaacctac agt 23

<210> 456
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 456
 ccttgaaaag gacccagttt 20

<210> 457
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 457
 atgagtcgca cctgctgttc cc 22

<210> 458
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 458
 tagcagctgc ccttggtta 18

<210> 459
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 459
 aacagcaggt gcgactcatt ta 22

<210> 460
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
 tgctaggcga cgacacccag acc 23

<210> 461
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 461
 tggacacgtg gcagtgga 18

 <210> 462
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 462
 tcatggtctc gtcccatc 19

 <210> 463
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 463
 taccattgt ttctctgtct ccccatc 27

 <210> 464
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 464
 caggcatcct tggagtag 18

 <210> 465
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 465
 tcccattag cacaggagta 20

 <210> 466

<211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 466
 aggcctcttgc ctgtcctgct gct 23

 <210> 467
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 467
 ggcacagagtc ccacttgt 18

 <210> 468
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 468
 actgctccgc ctactacga 19

 <210> 469
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 469
 aggcatactc gccgtcctca 20

 <210> 470
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 470
 aaggccaagg tgagtcacat 19

 <210> 471
 <211> 20
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

ccagtggtgtg cgaaacctaa 20

<210> 472

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 472

tcagggtcta catcagcttc ctgc 24

<210> 473

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

agggccagg tgagtccat 19

<210> 474

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

cctactgagg agccctatgc 20

<210> 475

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

tcagggtgga ccccaattca gg 22

<210> 476

<211> 24

<212> DNA

<213> Artificial Sequence

-220-

-223- Synthetic oligonucleotide probe

-240- 476

ggaggetta taggccaat ctgg 24

-210- 477

-211- 50

-212- DNA

-213- Artificial Sequence

-220-

-223- Synthetic oligonucleotide probe

-240- 477

ggcttcagca gcacgtgtga agtcgaagtc gcagtcacag atatcaatga 50

-230-

-1-